

## SEQUENCE LISTING

- <110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350  
<141> 2000-09-18
- <150> PCT/US00/04414  
<151> 2000-02-22
- <150> US 60/143,048  
<151> 1999-07-07
- <150> US 60/145,698  
<151> 1999-07-26
- <150> US 60/146,222  
<151> 1999-07-28
- <150> PCT/US99/20594  
<151> 1999-09-08
- <150> PCT/US99/20944  
<151> 1999-09-13

<150> PCT/US99/21090  
<151> 1999-09-15

<150> PCT/US99/21547  
<151> 1999-09-15

<150> PCT/US99/23089  
<151> 1999-10-05

<150> PCT/US99/28214  
<151> 1999-11-29

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28564  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/30911  
<151> 1999-12-20

<150> PCT/US99/30999  
<151> 1999-12-20

<150> PCT/US00/00219  
<151> 2000-01-05

<160> 423

<210> 1

<211> 1825

<212> DNA

<213> Homo sapiens

<400> 1

```
actgcacctc ggttctatcg attgaattcc ccgggggatcc tctagagatc cctcgacctc 60
gacccacgcg tccggggccgg agcagcacgg ccgcaggacc tggagctccg gctgcgtctt 120
cccgcagcgc taccgcgccat gcgcctgccg cgcggggccg cgctggggct cctgcccgtt 180
ctgctgctgc tgccgcccgc gccggaggcc gccaaagaagc cgacgccctg ccaccgggtg 240
cgggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300
ggcggaaca cggttgga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540
cccgactgtc tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg gtaccagggc 660
```

```

ccgctgtgca ctgactgcat ggacggctac ttcagctcgc tccggaacga gacccacagc 720
atctgcacag cctgtgacga gtcttgcaag acgtgctcgg gcctgaccaa cagagactgc 780
ggcgagtgtg aagtgggctg ggtgctggac gagggcgctt gtgtggatgt ggacgagtgt 840
gcgcccgagc cgctccctg cagcgctgcg cagttctgta agaacgcaa cggctcctac 900
acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag ggaagggccc aggaaactgt 960
aaagagtgtg tctctggcta cgcgaggag cacggacagt gtgcagatgt ggacgagtgc 1020
tcactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccagggagc 1080
tacgtctgtg tgtgtcctga cggcttcgaa gaaacggaag atgcctgtgt gccgccggca 1140
gaggctgaag ccacagaagg agaaagcccc acacagctgc cctcccgca agacctgtaa 1200
tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260
ggatgccgtc tcttgacgtg gacagcggcg gggagaggct gcctgctctc taacggttga 1320
ttctcatttg tcccttaaac agctgcattt cttggttgtt cttaaacaga cttgtatatt 1380
ttgatacagt tctttgtaat aaaattgacc attgtaggta atcaggagga aaaaaaaaaa 1440
aaaaaaaaaa aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500
gccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560
cacaaataaa gcattttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620
atcttatcat gtctggatcg ggaattaatt cggcgcagca ccatggcctg aaataacctc 1680
tgaaagagga acttggttag gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg 1740
tcagttaggg tgtggaaagt cccaggctc cccagcaggc agaagtatgc aagcatgcat 1800
ctcaattagt cagcaaccca gtttt 1825

```

<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
  1                      5                      10                      15

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
                20                      25                      30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
    35                      40                      45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
    50                      55                      60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
    65                      70                      75                      80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
                85                      90                      95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
    100                      105                      110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
    115                      120                      125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
    130                      135                      140

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
325 330 335

Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp  
340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

caggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatccctc tagagatccc 60  
tcgacctega cccacgcgtc cgccaggccg ggaggcgacg cggccagccg tctaaacggg 120  
aacagccctg gctgaggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
ggtgcggcac gaggagtttt ccggcagcg aggaggctct gacgagcatg gcccgaggga 240



```

ggcgccttccc tgccgcgcgcg ctctggctct ggagcatcct cctgtgcctg ctggcactgc 300
gggcggaggc cgggcgcgcg caggaggaga gcctgtacct atggatcgat gctcaccagg 360
caagagtact cataggattt gaagaagata tcctgattgt ttcagagggg aaaatggcac 420
cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480
attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540
ccttgcgctc cctggataaa ggcacatgag cagatccaac cgtcaatgtc cctctgctgg 600
gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtcct ggaaaacagg 660
atgggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720
tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780
gggtgccgaaa tggaggcttt tgtaatgaaa gacgcatctg cgagtgtcct gatgggttcc 840
acggacctca ctgtgagaaa gccctttgta cccacgatg tatgaatggg ggactttgtg 900
tgactcctgg tttctgcac tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960
actgctcaac cacctgcttt aatggaggga cctgtttcta ccctggaaaa tgtatttgcc 1020
ctccaggact agaggagag cagtgtgaaa tcagcaaatg cccacaacc tgtcgaaatg 1080
gaggtaaatg cattggtaaa agcaaatgta agtgttccaa aggttaccag ggagacctct 1140
gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaaccaaca 1200
aatgccaatg tcaagaagg tggcatggaa gacactgcaa taaaagggtac gaagccagcc 1260
tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgcct tcaactaaaa 1320
aggccgagga ggcgcgggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380
aaacgtttta agttacacca agttcatagc ctttgtaaac ctttcatgtg ttgaatgttc 1440
aaataatggt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag catgatggta 1560
tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcagggtta 1620
aaattttcag tgtgtagttg gcagatattt tcaaaattac aatgcattta tgggtgtctgg 1680
gggcagggga acatcagaaa ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg 1740
atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860
ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttacactgtg gtagtggcat 1920
ttaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980
gcattggctt gaagcaatat aatatattgt aaacaaaaca cagctcttac ctaataaaca 2040
ttttatactg tttgtatgta taaaataaag gtgctgcttt agttttttgg aaaaaaaaaa 2100
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgccgcg gactctagag tcgacctgca 2160
gaagcttggc cgccatggcc caacttgttt attgcagctt ataatg 2206

```

<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
  1             5             10             15

```

```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
      20             25             30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
      35             40             45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
      50             55             60

```

```

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

```

65					70					75				80	
Pro	Val	Asn	Ile	His	Ser	Met	Asn	Phe	Thr	Trp	Gln	Ala	Ala	Gly	Gln
				85					90					95	
Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly
			100					105					110		
Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro
		115					120					125			
His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
	130					135					140				
Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser	Glu
145					150					155					160
Gly	Asn	Thr	Ile	Leu	Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr
				165					170					175	
Cys	Gln	Gln	Ala	Glu	Cys	Pro	Gly	Gly	Cys	Arg	Asn	Gly	Gly	Phe	Cys
			180					185					190		
Asn	Glu	Arg	Arg	Ile	Cys	Glu	Cys	Pro	Asp	Gly	Phe	His	Gly	Pro	His
		195					200					205			
Cys	Glu	Lys	Ala	Leu	Cys	Thr	Pro	Arg	Cys	Met	Asn	Gly	Gly	Leu	Cys
	210					215					220				
Val	Thr	Pro	Gly	Phe	Cys	Ile	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Val	Asn
225					230					235					240
Cys	Asp	Lys	Ala	Asn	Cys	Ser	Thr	Thr	Cys	Phe	Asn	Gly	Gly	Thr	Cys
				245					250					255	
Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly	Glu	Gln
			260					265					270		
Cys	Glu	Ile	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly	Gly	Lys	Cys
	275						280					285			
Ile	Gly	Lys	Ser	Lys	Cys	Lys	Cys	Ser	Lys	Gly	Tyr	Gln	Gly	Asp	Leu
	290					295					300				
Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly	Ala	His	Gly	Thr	Cys
305					310					315					320
His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg	His
				325					330					335	
Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro	Ala
			340					345					350		

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
 370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 5

agggagcagc gacagtgtgc agatgtggac gagtgcac tagca 45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c 21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 7

taagtccggc acattacagg tc 22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 8

cccacgatgt atgaatggtg gactttgtgt gactcctggt ttctgcatc 49

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 9

aaagacgcat ctgcgagtgt cc

22

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 10

tgctgatttc acactgctct ccc

23

<210> 11

<211> 2197

<212> DNA

<213> Homo sapiens

<400> 11

cggacgcgtg	ggcgtccggc	ggtcgcagag	ccaggaggcg	gagggcgcgcg	ggccagcctg	60
ggccccagcc	cacaccttca	ccaggggcca	ggagccacca	tgtggcgatg	tccactgggg	120
ctactgctgt	tgtgccgct	ggctggccac	ttggctcttg	gtgccagca	gggtcgtggg	180
cgccgggagc	tagcacccgg	tctgcacctg	cggggcatcc	gggacgcggg	aggccggtac	240
tgccaggagc	aggacctgtg	ctgccgcggc	cgtgccgacg	actgtgccct	gccctacctg	300
ggcgccatct	gttactgtga	cctcttctgc	aaccgcacgg	tctccgactg	ctgccctgac	360
ttctgggact	tctgcctcgg	cgtgccaccc	ccttttcccc	cgatccaagg	atgtatgcat	420
ggaggtcgta	tctatccagt	cctgggaacg	tactgggaca	actgtaaccg	ttgcacctgc	480
caggagaaca	ggcagtggca	tgggtggatcc	agacatgata	aaagccatca	accagggcaa	540
ctatggctgg	caggctggga	accacagcgc	cttctggggc	atgaccctgg	atgagggcac	600
tcgctaccgc	ctgggcacca	tccgcccata	ttcctcggtc	atgaacatgc	atgaaattta	660
tacagtgtcg	aaccacaggg	aggtgcttcc	cacagccttc	gaggcctctg	agaagtggcc	720
caacctgatt	catgagcctc	ttgaccaagg	caactgtgca	ggctcctggg	ccttctccac	780
agcagctgtg	gcatacgata	gtgtctcaat	ccattctctg	ggacacatga	cgctgtcctt	840
gtcgccccag	aacctgctgt	cttgtgacac	ccaccagcag	cagggctgcc	gcgggtgggcg	900
tctcgatggg	gcctgggtgg	tcctgcgtcg	ccgaggggtg	gtgtctgacc	actgctaccc	960
cttctcgggc	cgtgaacgag	acgaggctgg	ccctgcgccc	ccctgtatga	tgcacagccg	1020
agccatgggt	cggggcaagc	gccaggccac	tgcccactgc	cccaacagct	atgttaataa	1080
caatgacatc	taccagggtca	ctcctgtcta	ccgcctcggc	tccaacgaca	aggagatcat	1140
gaaggagctg	atggagaatg	gccctgtcca	agccctcatg	gaggtgcatg	aggacttctt	1200
cctatacaag	ggaggcatct	acagccacac	gccagtgagc	cttgggaggc	cagagagata	1260
ccgcggcat	gggacccact	cagtcaagat	cacaggatgg	ggagaggaga	cgctgccaga	1320

```

tggaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggagagag 1380
gggccacttc cgcacgtgc gcggcgtcaa tgagtgcgac atcgagagct tcgtgctggg 1440
cgtctggggc cgcgtgggca tggaggacat gggcatcac tgaggctgag ggcaccacgc 1500
ggggtcgggc ctgggatcca ggctaagggc cggcggaaga ggccccaatg gggcggtgac 1560
cccagcctcg cccgacagag cccggggcgc aggcgggcgc cagggcgcta atcccggcgc 1620
gggttccgct gacgcagcgc cccgcctggg agcgcgggc aggcgagact ggcggagccc 1680
ccagacctcc cagtggggac ggggcagggc ctggcctggg aagagcacag ctgcagatcc 1740
caggcctctg gcgccccac tcaagactac caaagccagg acacctcaag tctccagccc 1800
caatacccca cccaatccc gtattctttt ttttttttt ttagacaggg tcttgctccg 1860
ttgcccaggt tggagtgcag tggcccatca gggctcactg taacctccga ctcctgggtt 1920
caagtgacct tcccacctca gcctctcaag tagctgggac tacagggtgca ccaccacacc 1980
tggctaattt ttgtattttt tgtaaagagg ggggtctcac tgtgttgccc aggtggttt 2040
cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgctg ggattgcagg 2100
catgagccac tgcaccacgc cctgtattct tattcttcag atattttatt ttcttttcac 2160
tgttttaaaa taaaaccaa gtattgataa aaaaaaa 2197

```

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly
  1                      5                      10                      15

```

```

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
      20                      25                      30

```

```

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35                      40                      45

```

```

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50                      55                      60

```

```

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65                      70                      75                      80

```

```

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85                      90                      95

```

```

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100                      105                      110

```

```

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115                      120                      125

```

```

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130                      135                      140

```

```

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
      145                      150                      155                      160

```

His Asp Pro Gly

<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (33)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (80)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (94)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (144)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (188)  
 <223> a, t, c or g

<400> 13  
 aggcctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcgtt gtctcaaadc 60  
 caattctctt gggacacatn acgcctgtcc tttngeccca gaacctgctg tcttgtacac 120  
 ccaccagcag cagggtctgc gcgntgggcg tctcgatggt gcctgggtgg tcttgcgtcg 180  
 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240  
 cctgcgccc cctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300  
 tgcccaactgc cccaacagct atgttaataa caatgacatc taccaggtca ctctgtcta 360  
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420  
 agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480  
 gccagtgagc cttgggaggc cagagagata ccgccggcat gggaccact cag 533

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc 24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15

ggcgtatct ctctggcctc cc 22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg 50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

```

gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcaactgcc tgctgtgcta 60
ctcctgcaaa gcccaggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120
gggggagcag tgctggaccg cgcgcacccg cgcagttggc ctccctgaccg tcatcagcaa 180
aggctgcagc ttgaactgcy tggatgactc acaggactac tacgtgggca agaagaacat 240
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggtgc 300
cgccatcctt gcgctgctcc ctgcactcgg cctgctgctc tggggacccg gccagctata 360
ggctctgggg gggcccgtg cagcccacac tgggtgtggg gcccagggc tctgtgccac 420
tcctcacaga cctggcccag tgggagcctg tcctggttcc tgaggcacat cctaaccgaa 480
gtctgaccat gtatgtctgc acccctgtcc cccaccctga ccctcccatg gccctctoca 540
ggactcccac ccggcagatc agctctagtg acacagatcc gcctgcagat ggcccctoca 600
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc cagggtctgg 720
ccgtgggtgc ccccgacccc agcaggggac aggcactcag gagggcccag taaaggctga 780
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900
aatggcagcc tgagcacagc gtaggcctt aataaacacc tgttgataa gccaaaaaaa 960

```

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctcctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

```

cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgcccc acctcactct 60
gtgcttacag ctgctgattc tctgctgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcaccg ggcgtcgcct ctccgccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacgtt tggcagcccg gttcgcatca aaggggctga 300
gagtgagaag tacatctgta tgaacaagag gggcaagctc atcgggaagc ccagcgggaa 360
gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg ccttccagaa 420
cgcccgccac gagggctggt tcatggcctt caccgcccag gggcgccccc gccaggcttc 480
ccgcagccgc cagaaccagc gcgaggccca cttcatcaag cgccctotacc aaggccagct 540
gcccttcccc aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgccccac 600
ccgcgggacc aagcgcacac ggcggcccca gcccctcacg tagtctggga ggcagggggc 660
agcagccctt gggccgcctc cccacccctt tcccttctta atccaaggac tgggctgggg 720
tggcgggagg ggagccagat ccccgaggga ggacctgag ggcgcgaag catccgagcc 780
cccagctggg aaggggcagg ccggtgcccc agggcgcggt ggcacagtgc ccccttccc 840
gacgggtggc aggccctgga gaggaactga gtgtcaccct gatctcaggc caccagcctc 900
tgccggcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg aaggccttgc 960
agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc tcggatctcc ctacgtctgc 1020
ccccagcccc caaactcctc ctggctagac tgtaggaagg gacttttgtt tgtttgtttg 1080
tttcaggaaa aaagaaaggg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140
acgaccaggg cctgcacccc acccccact cccagccccg gaataaaacc attttctctg 1200

```

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca

24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgctgctca nctggctcgg catggcgccc t

41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acctgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg ccttcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240  
 tatttttatt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300  
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420  
 gcttgacctc agtgcctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtgc gtgcacacgg 540  
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg gggtgctctt gccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720  
 gggccttcog ggaggctatt agcctcaaat tgttggtttt gtctaagaat cacctgagca 780  
 gtgtgcctgt tgggcttccct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840  
 ctgtcatatc cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900  
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
 aggaattttt aattgtacgt aattcgctgt cccaccctcc tcccgatctc ccaggtagcg 1020  
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

```

aagggggttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcatctctca 1260
acgtgcggggg tttcatgtgc caaggtcctg aacaagtccg ggggatggcc gtcagggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgacccccgg cctgcctctc ttcaccccag 1380
ccccaagtac agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440
gaagctacac gcctccaact cctaccacat cgaaacttcc cagattcctt gactgggatg 1500
gcagagaaaag agtgaccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca tacaaaactca 1620
catgggtgaa aatgggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttggt 1740
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggctcc ccttttctgc tggcgggctt gatcgggggc gcggtgatat 1920
ttgtgctggt ggtcttgctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaattgggg 2160
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacctgga gcactgccat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactcttg agaacacact cgtgtgtgca cataaagaca cgagattac atttgataaa 2340
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacggtg tactatataa 2400
tgggatttaa aaaaagtgc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaattctt

```

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1                      5                      10                      15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
                20                      25                      30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
    35                      40                      45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
    50                      55                      60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
    65                      70                      75                      80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                85                      90                      95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
    100                      105                      110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
    115                      120                      125

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

				405					410					415			
Val	Thr	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Gln	Leu	Ser	Ile	His	Phe	Val		
			420					425					430				
Asn	Asp	Thr	Ser	Ile	Gln	Val	Ser	Trp	Leu	Ser	Leu	Phe	Thr	Val	Met		
		435					440					445					
Ala	Tyr	Lys	Leu	Thr	Trp	Val	Lys	Met	Gly	His	Ser	Leu	Val	Gly	Gly		
	450					455					460						
Ile	Val	Gln	Glu	Arg	Ile	Val	Ser	Gly	Glu	Lys	Gln	His	Leu	Ser	Leu		
465				470					475						480		
Val	Asn	Leu	Glu	Pro	Arg	Ser	Thr	Tyr	Arg	Ile	Cys	Leu	Val	Pro	Leu		
				485					490					495			
Asp	Ala	Phe	Asn	Tyr	Arg	Ala	Val	Glu	Asp	Thr	Ile	Cys	Ser	Glu	Ala		
			500					505					510				
Thr	Thr	His	Ala	Ser	Tyr	Leu	Asn	Asn	Gly	Ser	Asn	Thr	Ala	Ser	Ser		
		515					520					525					
His	Glu	Gln	Thr	Thr	Ser	His	Ser	Met	Gly	Ser	Pro	Phe	Leu	Leu	Ala		
	530					535					540						
Gly	Leu	Ile	Gly	Gly	Ala	Val	Ile	Phe	Val	Leu	Val	Val	Leu	Leu	Ser		
545					550					555					560		
Val	Phe	Cys	Trp	His	Met	His	Lys	Lys	Gly	Arg	Tyr	Thr	Ser	Gln	Lys		
				565					570					575			
Trp	Lys	Tyr	Asn	Arg	Gly	Arg	Arg	Lys	Asp	Asp	Tyr	Cys	Glu	Ala	Gly		
			580					585					590				
Thr	Lys	Lys	Asp	Asn	Ser	Ile	Leu	Glu	Met	Thr	Glu	Thr	Ser	Phe	Gln		
		595					600						605				
Ile	Val	Ser	Leu	Asn	Asn	Asp	Gln	Leu	Leu	Lys	Gly	Asp	Phe	Arg	Leu		
	610					615					620						
Gln	Pro	Ile	Tyr	Thr	Pro	Asn	Gly	Gly	Ile	Asn	Tyr	Thr	Asp	Cys	His		
625					630					635					640		
Ile	Pro	Asn	Asn	Met	Arg	Tyr	Cys	Asn	Ser	Ser	Val	Pro	Asp	Leu	Glu		
				645					650					655			
His	Cys	His	Thr														
			660														

&lt;210&gt; 29

&lt;211&gt; 21

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggctctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacggggt gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcggcg gcggagacag aggcagaggc agaagctggg gtcctgtcct 60  
cgctccac gacgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

gaggaagacc	cgggtggctg	cgccctgcc	tcgcttccca	ggcgccggcg	gctgcagcct	180
tgcccctctt	gctcgcttg	aaaatggaaa	agatgctcgc	aggctgcttt	ctgctgatcc	240
tcggacagat	cgtcctctc	cctgccgagg	ccaggggagcg	gtcacgtggg	aggteccatct	300
ctaggggcag	acacgctcgg	acccacccgc	agacggccct	tctggagagt	tcctgtgaga	360
acaagcgggc	agacctggtt	ttcatcattg	acagctctcg	cagtgtcaac	acccatgact	420
atgcaaaggt	caaggagttc	atcgtggaca	tcttgcaatt	cttggacatt	ggtectgatg	480
tcacccaggt	gggctgctc	caatatggca	gcactgtcaa	gaatgagttc	tcctcaaga	540
ccttcaagag	gaagtccgag	gtggagcgtg	ctgtcaagag	gatgcggcat	ctgtccacgg	600
gcaccatgac	tgggctggcc	atccagtatg	ccctgaacat	cgcattctca	gaagcagagg	660
gggcccggcc	cctgaggagg	aatgtgccac	gggtcataat	gatcgtgaca	gatgggagac	720
ctcaggactc	cgtggccgag	gtggctgcta	aggcacggga	cacgggcata	ctaattcttg	780
ccattgggtg	gggccaggta	gacttcaaca	ccttgaagtc	cattgggagt	gagcccatg	840
aggaccatgt	cttccttggt	gccaatttca	gccagattga	gacgctgacc	tcctgtttcc	900
agaagaagtt	gtgcacggcc	cacatgtgca	gcaccctgga	gcataactgt	gccacttct	960
gcatcaacat	ccctggctca	tacgtctgca	ggtgcaaaaca	aggctacatt	ctcaactcgg	1020
atcagacgac	ttgcagaatc	caggatctgt	gtgccatgga	ggaccacaac	tgtgagcagc	1080
tctgtgtgaa	tgtgccgggc	tccttcgtct	gccagtgtca	cagtggctac	gccctggctg	1140
aggatgggaa	gaggtgtgtg	gctgtggact	actgtgcctc	agaaaaccac	ggatgtgaac	1200
atgagtgtgt	aaatgctgat	ggctcctacc	tttgccagtg	ccatgaagga	tttgctctta	1260
acccagatga	aaaaacgtgc	acaaggatca	actactgtgc	actgaacaaa	ccgggctgtg	1320
agcatgagt	cgtcaacatg	gaggagagct	actactgccg	ctgccaccgt	ggctacactc	1380
tggaccccaa	tggcaaaacc	tgcagccgag	tggaccactg	tgcacagcag	gaccatggct	1440
gtgagcagct	gtgtctgaac	acggaggatt	ccttcgtctg	ccagtgtcca	gaaggcttcc	1500
tcacaaacga	ggacctcaag	acctgctccc	gggtggatta	ctgacctgtg	agtgacctatg	1560
gttgtgaata	ctcctgtgtc	aacatggaca	gatcctttgc	ctgtcagttg	cctgagggac	1620
acgtgctccg	cagcgatggg	aagacgtgtg	caaaattgga	ctcttgtgct	ctgggggacc	1680
acggtttgtga	acattcgtgt	gtaagcagtg	aagattcggt	tgtgtgccag	tgctttgaag	1740
gttatatact	ccgtgaagat	ggaaaaacct	gcagaaggaa	agatgtctgc	caagctatag	1800
accatggctg	tgaacacatt	tgtgtgaaca	gtgacgactc	atacacgtgc	gagtgtttgg	1860
agggtattccg	gctcgtgag	gatgggaaac	gctgccgaag	gaaggatgtc	tgcaaatcaa	1920
cccaccatgg	ctgcgaacac	atttgtgtta	ataatgggaa	ttcctacatc	tgcaaatgct	1980
cagagggatt	tgttctagct	gaggacggaa	gacggtgcaa	gaaatgcact	gaaggcccaa	2040
ttgacctggt	ctttgtgatc	gatggatcca	agagtcttgg	agaagagaat	tttgaggctc	2100
tgaagcagtt	tgtcactgga	attatagatt	ccttgacaat	ttcccccaa	gccgctcgag	2160
tggggctgct	ccagtattcc	acacaggctc	acacagagtt	cactctgaga	aacttcaact	2220
cagccaaaga	catgaaaaaa	gccgtggccc	acatgaaata	catgggaaag	ggctctatga	2280
ctgggctggc	cctgaaacac	atgtttgaga	gaagttttac	ccaaggagaa	ggggccaggc	2340
ccctttccac	aagggtgcc	agagcagcca	ttgtgttcac	cgcaggacgg	gctcaggatg	2400
acgtctccga	gtgggccagt	aaagccaagg	ccaatgggtat	cactatgtat	gctgttgggg	2460
taggaaaagc	cattgaggag	gaactacaag	agattgcctc	tgagcccaca	aacaagcatc	2520
tcttctatgc	cgaagacttc	agcacaatgg	atgagataag	tgaaaaactc	aagaaaggca	2580
tctgtgaagc	tctagaagac	tccgatggaa	gacaggactc	tccagcaggg	gaactgccaa	2640
aaacgggtcca	acagccaaca	gaatctgagc	cagtcaccat	aaatatccaa	gacctacttt	2700
cctgtttctaa	ttttgcagt	caacacagat	atctgtttga	agaagacaat	cttttacggg	2760
ctacacaaaa	gctttcccat	tcaacaaaac	cttcaggaag	ccctttggaa	gaaaaacacg	2820
atcaatgcaa	atgtgaaaac	cttataatgt	tccagaacct	tgcaaacgaa	gaagtaagaa	2880
aattaacaca	gcgcttagaa	gaaatgacac	agagaatgga	agccctggaa	aatgcgctga	2940
gatacagatg	aagattagaa	atcgcgacac	atgtgtagtc	attgtatcac	ggattacaat	3000
gaacgcagtg	cagagcccca	aagctcaggc	tattgttaaa	tcaataatgt	tgtgaagtaa	3060
aacaatcagt	actgagaaac	ctggtttgcc	acagaacaaa	gacaagaagt	atacactaac	3120
ttgtataaat	ttatctagga	aaaaaatcct	tcagaattct	aagatgaatt	taccagggtga	3180
gaatgaataa	gctatgcaag	gtattttgta	atatactgtg	gacacaactt	gcttctgcct	3240
catcctgcct	tagtgtgcaa	tctcatttga	ctatacgata	aagtttgcac	agtcttactt	3300



ctgtagaaca ctggccatag gaaatgctgt ttttttgtac tggactttac cttgatatat 3360  
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420  
 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
 1 5 10 15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn Val	Pro Gly Ser Phe	Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
305	310	315	320			
Val Asp Tyr Cys	Ala Ser Glu Asn His	Gly Cys Glu His	Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
385	390	395	400			
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
465	470	475	480			
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500	505	510			

Gly 515	Tyr	Ile	Leu	Arg	Glu	Asp	Gly 520	Lys	Thr	Cys	Arg	Arg 525	Lys	Asp	Val
Cys 530	Gln	Ala	Ile	Asp	His	Gly 535	Cys	Glu	His	Ile	Cys 540	Val	Asn	Ser	Asp
Asp 545	Ser	Tyr	Thr	Cys	Glu 550	Cys	Leu	Glu	Gly	Phe 555	Arg	Leu	Ala	Glu	Asp 560
Gly	Lys	Arg	Cys	Arg 565	Arg	Lys	Asp	Val	Cys 570	Lys	Ser	Thr	His	His 575	Gly
Cys	Glu	His	Ile 580	Cys	Val	Asn	Asn	Gly 585	Asn	Ser	Tyr	Ile	Cys 590	Lys	Cys
Ser	Glu	Gly 595	Phe	Val	Leu	Ala	Glu 600	Asp	Gly	Arg	Arg	Cys 605	Lys	Lys	Cys
Thr	Glu 610	Gly	Pro	Ile	Asp	Leu 615	Val	Phe	Val	Ile	Asp 620	Gly	Ser	Lys	Ser
Leu 625	Gly	Glu	Glu	Asn	Phe 630	Glu	Val	Val	Lys	Gln 635	Phe	Val	Thr	Gly	Ile 640
Ile	Asp	Ser	Leu 645	Thr	Ile	Ser	Pro	Lys	Ala 650	Ala	Arg	Val	Gly	Leu 655	Leu
Gln	Tyr	Ser	Thr 660	Gln	Val	His	Thr	Glu 665	Phe	Thr	Leu	Arg	Asn 670	Phe	Asn
Ser	Ala	Lys 675	Asp	Met	Lys	Lys	Ala 680	Val	Ala	His	Met	Lys 685	Tyr	Met	Gly
Lys	Gly 690	Ser	Met	Thr	Gly	Leu 695	Ala	Leu	Lys	His	Met 700	Phe	Glu	Arg	Ser
Phe 705	Thr	Gln	Gly	Glu	Gly 710	Ala	Arg	Pro	Leu	Ser 715	Thr	Arg	Val	Pro	Arg 720
Ala	Ala	Ile	Val	Phe 725	Thr	Asp	Gly	Arg	Ala 730	Gln	Asp	Asp	Val	Ser 735	Glu
Trp	Ala	Ser	Lys 740	Ala	Lys	Ala	Asn	Gly 745	Ile	Thr	Met	Tyr	Ala 750	Val	Gly
Val	Gly	Lys 755	Ala	Ile	Glu	Glu	Glu 760	Leu	Gln	Glu	Ile	Ala 765	Ser	Glu	Pro
Thr	Asn 770	Lys	His	Leu	Phe	Tyr 775	Ala	Glu	Asp	Phe	Ser 780	Thr	Met	Asp	Glu
Ile 785	Ser	Glu	Lys	Leu	Lys 790	Lys	Gly	Ile	Cys	Glu 795	Ala	Leu	Glu	Asp	Ser 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
                     805                    810                    815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
                     820                    825                    830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
                     835                    840                    845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
                     850                    855                    860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
                     865                    870                    875                    880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
                     885                    890                    895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
                     900                    905                    910

Arg Tyr Arg  
                     915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                     oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

```

ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt cgcgagcct 60
cggcacctgc aggtccgtgc gtcccgcggc tggcgccctt gactccgtcc cggccaggga 120
gggccatgat ttccctcccg gggccccctg tgaccaactt gctgcggttt ttgttcctgg 180
ggctgagtgc cctcgcgccc ccctcgcggg ccagctgca actgcacttg cccgccaacc 240
ggttgcaggc ggtggaggga ggggaagtgg tgcttcagc gtggtacacc ttgcacgggg 300
aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaaag 360
aaaaggagga tcagggtgtt tctacatca atggggtcac aacaagcaaa cctggagtat 420
ccttggtcta ctccatgccc tcccggaacc tgctccgtcg gctggagggt ctccaggaga 480
aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccactctgcc 600
gtctccaggg tgtgccccat gtgggggcaa acgtgacctt gagctgccag tctccaagga 660
gtaagccgcg tgtccaatac cagtgggatc ggcagcttcc atccttcag actttctttg 720
caccagcatt agatgtcatc cgtgggtctt taagcctcac caacctttcg tcttccatgg 780
ctggagtcta tgtctgcaag gccacacaat aggtgggcac tgcccaatgt aatgtgacgc 840
tggaagtgag cacagggcct ggagctgcag tggttgctgg agctgttgtg ggtaccctgg 900
ttggactggg gttgctggct gggctgggtc tcttgtaaca ccgcccgggc aaggccctgg 960
aggagccagc caatgatata aaggaggatg ccattgctcc ccggacctg ccctggccca 1020
agagctcaga cacaatctcc aagaatggga ccttttctc tgtcacctcc gcacgagccc 1080
tccggccacc ccatggccct cccaggcctg gtgcattgac cccacgccc agtctctcca 1140
gccaggccct gccctcacca agactgccc cgacagatgg gggccacct caaccaatat 1200
cccccatccc tgggtggggtt tcttctctcg gcttgagcgg catgggtgct gtgctgtga 1260
tgggtgcctg ccagagtcaa gctggctctc tggatgatg accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tctataagg gtcacctcta gcacagaggc ctgagtcag 1380
ggaaagagtc aactcctga cccttagtac tctgccccca cctctcttta ctgtgggaaa 1440
accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
attgggagga gctccacccc acccctgact cctccttatg aagccagctg ctgaaattag 1560
ctactacca agagtgaggg gcagagactt ccagtcactg agtctcccag gccccttga 1620
tctgtacccc acccctatct aacaccaccc ttggtccca ctccagctcc ctgtattgat 1680
ataacctgtc aggctggctt ggtaggttt tactggggca gaggataggg aatctcttat 1740
taaaactaac atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800
tttgtatgaa aaa
1813

```

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50

<210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 43  
 gtgtgacaca gcgtgggc 18

<210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 44  
 gaccggcagg cttctgcg 18

<210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 45  
 cagcagcttc agccaccagg agtgg 25

<210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 46  
 ctgagccgtg ggctgcagtc tcgc 24

<210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 cgccaccact gcggccaccg ccaatgaaac gcctcccgtc cctagtgggt ttttccactt 60  
 tggtgaattg ttcctatact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120  
 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagtattt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcc a tttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
 taggttacaa gaacaacact atctcagcca aggacaccct ttctaactca actcttactg 600  
 aatttgtaaa aaccgtgaat aattttgttc aaagggtatc atttgtagtt tgggacaagt 660  
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720  
 ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780  
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840  
 atattggatg agactacata aatatatttc caaagagaaa agctgcatat gattcaaagt 900  
 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960  
 acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttcagtaat ttcagtctca atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080  
 taacatttac attaagtcac cgaaagggtc cagataggta taggagtcta tgtgcatttt 1140  
 ggaattactc acctgatacc atgaatggca gctggtcttc agagggtgtg gagctgacat 1200  
 actcaaatga gaccacacc tcatgccgtc gtaatcacct gacacatttt gcaattttga 1260  
 tgcctctctg tccttccatt ggtattaaag attataatat tcttacaagg atcactcaac 1320  
 taggaataat tatttctactg atttgccttg ccatatgcat ttttaccttc tgggtcttca 1380  
 gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440  
 ctgaacttgt ttttcttggt gggatcaata caaatactaa taagctcttc tgttcaatca 1500  
 ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560  
 tacatctcta tctcattgtt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620  
 tttatatctt tggtatctta agcccagccg tggtagtgtg attttcggca gcaactaggat 1680  
 acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaacaac tttatttggga 1740  
 gttttatagg accagcatgc ctaatcattt ttgttaatct cttggctttt ggagtcacat 1800  
 tatacaaaag ttttcgtcac actgcagggt tgaaccaga agttagtgtc tttgagaaca 1860  
 taagggtcttg tgcaagagga gccctcgctc ttctgttctt tctcgccacc acctggatct 1920  
 ttggggttct ccatgttgtg cagcatcagc tggttacagc ttacctcttc acagtcagca 1980  
 atgctttcca ggggatgttc atttttttat tctgtgtgtt tttatctaga aagattcaag 2040  
 aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100  
 agagaatggt ggataattac aactgcacaa aaataaaaaa tccaagctgt ggatgaccaa 2160

```

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtatttttaa 2220
atcagttttt ctgtttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
ggaaagtaat tggttttctca ggagtगतat cactgcaccc aaggaaagat tttctttcta 2400
acacgagaag tatatgaatg tcctgaagga aaccactggc ttgatatttc tgtgactcgt 2460
gttgcctttg aaactagtc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
cataagagaa tgaaggggca gaatatcaaa cagtgaaaag ggaatgataa gatgtatttt 2580
gaatgaactg ttttttctgt agactagctg agaaattgtt gacataaaat aaagaattga 2640
agaaacacat tttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700
agactttctg ttgctaaatc tgttttcttt tctaataattc taaaaaaaaa aaaaagggtt 2760
acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa 2822

```

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
 1              5              10              15

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100             105             110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115             120             125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130             135             140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145             150             155             160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165             170             175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

[illegible]

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480  
 Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495  
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510  
 Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525  
 Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540  
 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560  
 Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575  
 Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590  
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605  
 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620  
 Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640  
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655  
 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670  
 Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685  
 Leu Arg  
 690  
 <210> 50  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> modified\_base  
 <222> (61)

<223> a, t, c or g

<400> 50

```

tggaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaattggca atgttgcagt tgcattttta tattataaga 120
gtattggtcc ctttgctttc atcatctgac aaattcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacg aaaggtcaca 300
gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggctctcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta ttactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc tgggcggggg caccgccggt 120

```

gggacaagaa gccgcgcgct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240
tgctcgggtg tcttgggcac ctaccggtgg ggcccgtaa ggcgtactat ataaggctgc 300
cggcccgag cggccgcgcc gtcagagcag gagcgtgcg tccaggatct agggccacga 360
ccatcccaac cgggcactca cagcccgcga gcgcataccg gtcgccgccc agcctcccgc 420
acccccatcg cgggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gcccctcgc 540
cttctcggac gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600
cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcaccc gtgccgacgg 660
cgtcgtggac tgcgcgcggg gccagagcgc gcacagtttg ctggagatca aggcagtcgc 720
tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgccga 780
cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840
ccgccagat ggctacaatg tgtaccgatc cgagaagcac cgctcccgg tctccctgag 900
cagtgcctaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatcttct 960
gcccattgctg cccatggtcc cagaggagcc tgaggacctc aggggccact tggaaatctga 1020
catgtttctc tcgcccctgg agaccgacag catggaccca tttgggcttg tcaccggact 1080
ggaggccgtg aggagtccta gctttgagaa gtaactgaga ccatgcccg gctcttcac 1140
tgctgccagg ggctgtggtta cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200
agtccacgtt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260
tccattggca gtgccagttt ctagccaata gacttgctg atcataacat tgtaaagcctg 1320
tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380
gctgcactgt ctcatgtctg cttgaatacc tccatcgatg gggaaactcac ttcttttga 1440
aaaattctta tgtcaagctg aaattctcta attttttctc atcacttccc caggagcagc 1500
cagaagacag gcagtagttt taatttcagg aacagggtgat ccactctgta aaacagcagg 1560
taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
cccttcccaa atccctccag gccagaactg actggagcag gcattggcca ccaggcttca 1680
ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa tccccctga 1740
ggccagttct gtcattggatg ctgtcctgag aataaactgc tgtcccggtg tcacctgctt 1800
ccatctccca gccaccagc cctctgcca cctcacatgc ctccccatgg attggggcct 1860
cccaggcccc ccaccttatg tcaacctgca cttcttgttc aaaaatcagg aaaagaaaag 1920
atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacct 1980
gaacccttcc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgcccccaa ttatatttat gtatgtaagt 2100
gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

```

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1                      5                      10                      15

```

```

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
                20                      25                      30

```

```

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
    35                      40                      45

```

```

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
    50                      55                      60

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 60

atccgcccag atggctacaa tgtgta

26

&lt;210&gt; 61

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 61

gcctcccggc ctccctgagc agtgccaaac agcggcagtg ta

42



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggcgccct gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggcctatt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtggag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgatttttaa aatcgagctg agatgataga 360  
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatata gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaagtatt 480  
 agtgggtcca gcagtccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaagggaa tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggtcccaa agcaccaaca gctcatacac 660  
 aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720  
 atattcctgt gaagcccga attctgttgg atatcgcagg tgtcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggccttgggt tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctcttccag aagagtaatt ctcatctaa agccacgaca atgagtgaat atgtgcagtg 960  
 gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcga gcctgggtta 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
           35                          40                          45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
           50                          55                          60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
           65                          70                          75                          80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                           85                          90                          95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                           100                          105                          110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
                           115                          120                          125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
           130                          135                          140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
           145                          150                          155                          160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                           165                          170                          175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                           180                          185                          190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
           195                          200                          205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
           210                          215                          220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
           225                          230                          235                          240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                           245                          250                          255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
                           260                          265                          270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
           275                          280                          285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
           290                          295                          300  
 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

&lt;210&gt; 65

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 65

atcgttggtga agttagtgcc cc

22

&lt;210&gt; 66

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 66

acctgcgata tccaacagaa ttg

23

&lt;210&gt; 67

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

&lt;210&gt; 68

&lt;211&gt; 2639

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaag 60  
agaaagaaga ggaagatggt gggcaacatt tatttaacat gctccacagc cgggaccctg 120  
gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
aaataaatga attactcaat ctccatgac catctataca tactccacct tcaaaaagta 240  
catcaaatatt atatcattaa ggaaatagta acctctctt ctccaatatg catgacattt 300  
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtgggttcta 360  
tggcattcat catttgacaa atgcaagcat cttccttata aatcagctcc tattgaactt 420  
actagcactg actgtggaat cottaagggc ccattacatt tctgaagaag aaagctaaga 480  
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtag 540

```

aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggt 600
ttacaccag atccatttat atggaagcat ctacagtga ttgtaatgat ttaggtcttt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcttttctg 840
tgtacctaga ggaaaacaaa cttactgaac tgctgaaaa atgtctgtcc gaactgagca 900
acttacaaga actctatatt aatcacaaact tgctttctac aatttcacct ggagccttta 960
ttggcctaca taatcttctt cgacttcac tcaattcaaa tagattgcag atgatcaaca 1020
gtaagtgggt tgatgctctt ccaaactctag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac tttaaagctc ttatcaatct tgcagcctg gttatagctg 1140
gtataaacct cacagaaata ccagataacg ccttggttg actggaaaac ttagaaagca 1200
tctcttttta cgataacagg cttattaaag taccatgtg tgctcttcaa aaagttgtaa 1260
atctcaaatt tttggatcta aataaaaaatc ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacccta 1440
gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcaactcatgc 1500
tgaacagcaa tgctctcagt gccctgtacc atggtaccat tgagtctctg ccaaacctca 1560
aggaaatcag catacacagt aaccccatca ggtgtgactg tgtcatcctg tggatgaaca 1620
tgaacaaaac caacattcga ttcattggagc cagattcact gttttgcgtg gaccacctg 1680
aattccaagg tcagaatgtt cggcaagtgc atttcaggga catgatggaa atttgtctcc 1740
ctcttatagc tcctgagagc tttccttcta atctaaatgt agaagctggg agctatgttt 1800
cctttcactg tagagctact gcagaaccac agcctgaaat ctactggata acaccttctg 1860
gtcaaaaact cttgcctaata accctgacag acaagttcta tgtccattct gagggaacac 1920
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgata gcaactaacc 1980
tagttggcgc tgacttgaag tctgttatga tcaaagtga tggatctttt ccacaagata 2040
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100
ggaaagcaag ttctaaaatt ctcaaatcta gtgttaaagt gacagccttt gtcaagactg 2160
aaaattctca tgctgcgcaa agtgctcgaa taccatctga tgtcaaggta tataatctta 2220
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280
aaaacagaaa aaaatgtgta aatgtcacca ccaaagggtt gcaccctgat caaaaagagt 2340
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400
gtgtgatatg tcttatcagc tgctctctc cagaaatgaa ctgtgatggg ggacacagct 2460
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520
taaattctct ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

```

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

```

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
  1                      5                      10                      15

```

```

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
          20                      25                      30

```

```

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
  35                      40                      45

```

```

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
  50                      55                      60

```

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

	340		345		350										
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
	355						360					365			
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
	370						375					380			
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
385					390					395					400
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
			420					425						430	
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
		435					440					445			
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
	450					455						460			
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
465					470					475					480
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
				485					490						495
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
			500					505						510	
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
	515						520						525		
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
	530					535						540			
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
545					550					555					560
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565					570					575	
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys
			580					585						590	
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn
	595						600						605		
Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn
	610					615							620		

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

```

gcccgggact ggcgcaaggt gcccagcaa ggaaagaaat aatgaagaga cacatgtgtt 60
agctgcagcc ttttgaaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120
ttaccacgct tgttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taaccogtto cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300
ttcctctggg gggttaaagt tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360
tcttctcctt gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420
tgaaatTTTT aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600
aattgccaac aaccctggc actgogactg tactctacag caagttctga ggagcatggc 660
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720
tggcagacca ttctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaac 780
taccgattat gccatgctgg tcaccatggt tggctgggtc actatggtga tctcatatgt 840
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080
tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140
caccctttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcaactattta ataatgaaat ttattttttt aattttaaag caaataaaag 1260
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

```

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

accgagccga gcggaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtag gagcatgcc agccccctcc tggcctgctg gcagcccatc ctctgctgg 120
tgctgggctc agtgctgtca ggctcggcca cgggctgccc gcccgcgtgc gaggctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggagtcctcc gagggcatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagccccg cgccttcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgtca ggctcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctactgg actacatggt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacagcct ggagcagctg acgtggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgctc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctcttcaag aggtgtacc gactcaagggt cttggagatc tcccactggc 780
cctacttga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggccgt ccgccacctg gtctatctcc 900
gcttcctcaa cctctctac aaccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctgggtg gcgggcagct ggcggtggtg gagecctatg 1020
ccttcgcggg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tggaggaatc agtcttccac tcggtgggca acctggagac actcatctcg gactccaacc 1140
cgctggcctg cgactgtcgg ctctgtggg tgttcggcg ccgctggcgg ctcaacttca 1200
accggcagca gccacgtgc gccacgccc agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgcc aactacttca cctgcgcgc cgcccgcatc cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacgggtgca gtttgtgtgc cgggcccgatg 1380
gcgaccgcgc gcccgccatc ctctggctct caccocgaaa gcacctggtc tcagccaaga 1440
gcaatgggcy gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gccaggtac 1500
aggacaacgg cacgtacctg tgcacgcgg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgccc actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag agggcaacag caccgcgcgc actgtgcctt 1680
tccccttga catcaagacc ctcatcatcg ccaccacct gggcttcatc tctttcctgg 1740
gcgtcgtcct cttctgcctg gtgctgctgt ttctctggag ccgggggcaag ggcaacacaa 1800
agcaacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggcatc agctccgccg 1860
acgcgccccg caagttcaac atgaagatga tatgagccg gggcgggggg cagggaacccc 1920
cgggcggccg ggcaggggaa ggggcctggt cgccacctgc tcaactctca gtccttccca 1980
cctcctccct acccttctac acacgttctc tttctccctc ccgcctccgt cccctgctgc 2040
cccccgccag ccctcaccac ctgcctcct tctaccagga cctcagaagc ccagacctgg 2100
ggaccccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaaa
2290

```

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30  
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

	580		585		590										
Ile	Glu	Ile	Glu	Tyr	Val	Pro	Arg	Lys	Ser	Asp	Ala	Gly	Ile	Ser	Ser
	595						600					605			
Ala	Asp	Ala	Pro	Arg	Lys	Phe	Asn	Met	Lys	Met	Ile				
	610					615					620				

&lt;210&gt; 74

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 74

tcacctggag cctttattgg cc

22

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 75

ataccagcta taaccaggct gcg

23

&lt;210&gt; 76

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg  
gg

50

52

&lt;210&gt; 77

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 77  
 ccatgtgtct cctcctacaa ag 22

<210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
 gggaatagat gtgatctgat tgg 23

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 79  
 cacctgtagc aatgcaaadc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 80  
 agcaaccgcc tgaagctcat cc 22

<210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 81  
 aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cggggggcgcc ctttcgggtca 60  
 acatcgtagt ccacccccctc cccatcccca gcccccgagg attcaggctc gccagcgccc 120  
 agccaggag cgggcccggg agcgcgatgg gggccccagc cgcctcgtc ctgctcctgc 180  
 tcctgctgtt cgcctgctgc tgggcgcccg gcggggccaa cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaaccg tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct gggtacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcactat gcctgtgcga actgccagt cctcgtcac tgtgctagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggg gaccaagaac 660  
 tccacggaga accaaccgct atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gctcggtgac attccagggt acccgggagg atgatggggc gagcatcgtg tgctctgtga 780  
 accatgaatc tctaaagggg gctgacagat ccacctctca acgcattgaa gttttataca 840  
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgagggccag aagctgttgc 900  
 tacactgtga gggtcgcggc aatccagtcc cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgccctgat ctccctttc ctcaacaaga 1020  
 gtgacagtgg cactacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgtaaatgac cccagtccgg tgccctcctc ctccagcacc taccacgcca 1140  
 tcatcggtgg gatcgtggct ttcatgtgtc tcctgctgct catcatgctc atcttccttg 1200  
 gccactactt gatccggcac aaaggaacct acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320  
 acaagaagga atatttcac tagaggcgcc tgcccacttc ctgcgcccc caggggccct 1380  
 gtggggactg ctggggccgt caccaccccg gacttgtaca gagcaaccgc agggccgccc 1440  
 ctcccgttg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgctgt 1500  
 tttgtactcg gtttggaatg gggagggagg agggcggggg gaggggaggg ttgccctcag 1560  
 ccctttccgt ggcttctctg catttgggtt attattattt ttgtaacaat cccaaatcaa 1620  
 atctgtctcc aggctggaga ggcaggagcc ctgggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

&lt;400&gt; 87

cctagcacag tgacgagga cttggc

26

&lt;210&gt; 88

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 88

aagacacagc caccctaaac tgtagctctt ctgggagcaa gcctgcagcc

50

&lt;210&gt; 89

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt

50

&lt;210&gt; 90

&lt;211&gt; 2755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

```

gggggttagg gaggaaggaa tccaccccca ccccccaaa cccttttctt ctcttttctt 60
ggcttcggac attggagcac taaatgaact tgaatttgtt ctgtggcgag caggatgggtc 120
gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180
tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240
agagaagatc tgttcctgca atgagataga aggggacctc cacgtagact gtgaaaaaaaa 300
gggcttcaca agtctgcagc gtttctactgc cccgacttcc cagttttacc atttatttct 360
gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggt 420
tagtttgcac atggaaaaca atggcttgca tgaaatcggt ccgggggctt ttctggggct 480
gcagctgggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540
ttttctgggg ctggacgatc tgggaatatct ccaggctgat ttttaatttat tacgagatat 600
agacccgggg gccttccagg acttgaacaa gctggagggtg ctcatatttaa atgacaatct 660
catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tgcacctccg 720
gggtaacagg ctgaaaacgc tgccctatga ggaggcttg gagcaaatcc ctggtattgc 780
ggagatcctg ctagaggata acccttggga ctgcacctgt gatctgctct ccctgaaaga 840
atggctggaa aacattccca agaatgccct gatcgccga gtggtctgct aagccccac 900
cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960
ccgagtggat tctagtctcc cggcgccccc tgcccagaa gagaccttg ctctggacc 1020
cctgccaaact cctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

```

```

aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140
agcgacgggt agctccagga acaaaccctt agctaacagt ttaccctgcc ctgggggctg 1200
cagctgcgac cacatcccag ggtcgggttt aaagatgaac tgcaacaaca ggaacgtgag 1260
cagcttggct gatttgaagc ccaagctctc taacgtgcag gagcttttcc tacgagataa 1320
caagatccac agcatccgaa aatcgcactt tgtggattac aagaacctca ttctgttgga 1380
tctgggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttgacct 1440
caggtggcta tacatggata gcaattacct ggacacgctg tcccgggaga aattcgcggg 1500
gtcgcaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctcccggg 1560
cactttcaat gccatgcccc aactgaggat cctcattctc aacaacaacc tgctgaggtc 1620
cctgcctgtg gacgtgttcg ctggggtctc gctctctaaa ctacgctgc acaacaatta 1680
cttcatgtac ctcccgttg gagggtgct ggaccagtta acctccatca tccagataga 1740
cctccacgga aaccctggg agtgctcctg cacaattgtg cctttcaagc agtgggcaga 1800
acgcttgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgccgg tgaacttctt 1860
tagaaaaggt ttcattgctc tctccaatga cgagatctgc cctcagctgt acgctaggat 1920
ctcgcccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga ccgggacgca 1980
ctccaaactc tacctagaca ccagcagggt gtccatctcg gtgttggtcc cgggactgct 2040
gctggtgttt gtcacctccg ccttcaccgt ggtgggcatg ctctgttcta tcctgaggaa 2100
ccgaaagcgg tccaagagac gagatgccaa ctctcccgcg tccgagatta attccctaca 2160
gacagtctgt gactcttcct actggcaca tgggccttac aacgcagatg gggcccacag 2220
agtgtatgac tgtggctctc actcgctctc agactaagac cccaaccca ataggggagg 2280
gcagagggaa ggcgatacat ccttcccac cgcaggcacc ccgggggctg gaggggcgtg 2340
tacccaaact cccgcgcat cagcctggat gggcataagt agataaataa ctgtgagctc 2400
gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
tggagagctg ggagagcgca gccagctcgc tctttgctga gagccccttt tgacagaaag 2520
cccagcacga ccctgctgga agaactgaca gtgccctcgc cctcgggccc ggggcctgtg 2580
gggttggatg ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640
atatctattt ttcccctgtg gattagcccc gtgatggctc cctgttggct acgcagggat 2700
gggcagtgtc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755

```

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala  
1 5 10 15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn  
20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

	660	665	670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp			
	675	680	685
Cys Gly Ser His Ser Leu Ser Asp			
	690	695	
<210>	92		
<211>	22		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Description of Artificial Sequence: Synthetic		
	oligonucleotide probe		
<400>	92		
gttggatctg ggcaacaata ac			22
<210>	93		
<211>	24		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Description of Artificial Sequence: Synthetic		
	oligonucleotide probe		
<400>	93		
attgttgatgc aggctgagtt taag			24
<210>	94		
<211>	45		
<212>	DNA		
<213>	Artificial Sequence		
<220>			
<223>	Description of Artificial Sequence: Synthetic		
	oligonucleotide probe		
<400>	94		
ggcggctata catggatagc aattacctgg acacgctgtc ccggg			45
<210>	95		
<211>	2226		
<212>	DNA		
<213>	Homo sapiens		
<400>	95		
agtcgactgc gtcccttgta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60			
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgcggcctaa gggaaaactgt 120			
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgctcggg agcgagggcg 180			

```

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaatgaggg cggcggtcgc cctgtgcctc ctctggcagg cgctctggcc 360
cgggccggggc ggcggcgaac accccactgc cgaccgtgct ggctgctcgg cctcgggggc 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcaccc 480
gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540
cctcggggca ggcccagggg ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600
ggagcgcagg cgttccact gcacctgga gaacgagcct ttgcgggggt tctcctggct 660
gtcctccgac ccggcggtc tcgaaagcga cacgtgcag tgggtggagg agccccaacg 720
ctcctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggctg agcccgagg 780
ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840
ggtcttgtgt cctgcgcgcg gccccggggc cgctctaac ttgagctatc gcgcgcctt 900
ccagctgcac agcgccgctc tggacttcag tccacctggg accgaggtga gtgcgctctg 960
ccggggacag ctcccgatct cagttaactg catcgcgag gaaatcggcg ctcgctggga 1020
caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctccgtg ctggcaaagt 1080
cgagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140
cttcgagctg ggggaaggac gccgctcttg tgtgaccagt ggggaaggac agccgacct 1200
tggggggacc ggggtgccca ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260
gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320
agacaattca gtaacatcta ttcctgagat tctcgtatgg ggatcacaga gcacgatgtc 1380
tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccccat cagggagcgt 1440
gatttccaag ttttaattcta cgacttcctc tgccactcct caggctttcg actcctcctc 1500
tgccgtggtc ttcataattg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560
agtactgggg ctgttcaagc tctgctttca cgaaagcccc tcttccagc caaggaagga 1620
gtctatgggc ccgcccggcc tggagagtga tctgagccc gctgctttgg gctccagttc 1680
tgcacattgc acaaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740
gggtgccttg ctggcgagat cccctcttgg ctctagtgat gcatagggaa acaggggaca 1800
tgggcactcc tgtgaacagt ttttcacttt tgatgaaacg ggggaaccaag aggaacttac 1860
ttgtgtaact gacaatttct gcagaaatcc cccttcctct aaattccctt tactccactg 1920
aggagctaaa tcagaactgc aactccttc cctgatgata gaggaagtgg aagtgccttt 1980
aggatgggta tactggggga ccgggtagtg ctggggagag atattttctt atgtttattc 2040
ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctaccaa atggaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220
gttgat
2226

```

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

```

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
  1                      5                      10                      15

```

```

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
                20                      25                      30

```

```

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
    35                      40                      45

```

```

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
    50                      55                      60

```

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395 400
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
	405	410 415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
	420	425 430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
	435	440 445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
	450	455 460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
	465	470 475 480
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
	485	490

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgatgcca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20



<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 99  
 acagagcaga gggcgccttg

20

<210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 100  
 tcagggacaa gtggtgtctc tccc

24

<210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 101  
 tcagggaagg agtgtgcagt tctg

24

<210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 102  
 acagctcccg atctcagtta cttgcacgc ggacgaaac ggcgctcgct

50

<210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

```

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatcccccggt ctacctgggc cgccccgcgg cggtgcgcgc gtgagagggg gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtgtgt gccagtgtga gcggcggtgt gagcgcggtg 240
ggtgccgagg ggcgtgtgtg ccggcgcgcg cgccgtgggg tgcaaaccac gagcgtctac 300
gctgccatga ggggcgcgaa cgcctgggcg ccaactctgcc tgcctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gatttatttg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttggg aaatcacagt tcccgaaggg aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaac cagctggcaa tggcttcatt 720
gccatgttct ccgctgtctga accaaacgaa agagggggatc agtattgtgg aggactcctt 780
gacagacctt ccggctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840
gtcacttgtg tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960
ggggaagtca acgatgctag aagaattgga agtattgtg gtgatagtc accctgcgcca 1020
atttgtctg agagaaatga acttcttatt cagtttttat cagacttaag tttactgca 1080
gatgggttta ttggtcacta catattcagg ccaaaaaaac tgcctacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg gggtttaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaaac catcactcgc gatgggagtt tgacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg tcgtctgcaa gcagtgcctt ctctcagaa gaggtctaaa ttacattatt 1440
atgggccaag taggtgaaga tgggcgagggc aaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca tttaagctgt attctgccat tgcccttgaa agatctatgt tctctcagta 1620
gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactcttc acatgatgga ggtatgaggc ctccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttgga gcgtttattt atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1              5              10              15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

	340		345		350										
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro
	355						360				365				
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu
	370					375					380				
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys
385					390				395						400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys	
			405						410					415	

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105

cgcattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

```

cggacgcgtg ggccggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctccagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggg tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgctggggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgcctgctgg agctgagtga ggagctgggt gagagctggg ggtttcacia gcagcaggag 480
gccccggacc tcttccagtg gctgtgctca gattccctga agctctgctg ccccgaggc 540
accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cgggtggctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc ccctgtgccc gatgctcagg acctgaggaa 780
tcaaactggt tgcaatgcaa gaagggtcgg gccctgcctc acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgctg gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaaag gcctgcctag gctgcatggg ggcagggcca 960
ggtcgctgta agaagtgtag ccctggctat cagcaggtgg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcatctgtgc cgagggtac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taaggcgac 1260
ttggtgttca ccgccatctt cattggggct gtggcggcca tgactggcta ctggttgtca 1320
gagcgcagtg accgtgtgct ggagggtctc atcaagggca gataatcgcg gccaccacct 1380
gtaggacctc ctcccaccca cgctgcccc agagcttggg ctgccctcct gctggacact 1440
caggacagct tggtttattt ttgagagtgg ggtaaagacc cctacctgcc ttacagagca 1500
gcccaggtag ccaggccccg gcagacaagg cccctggggt aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttctt taatggtggc tgctagagct ttggcccctg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gtcctcctc gccagctgca tgctgccagt tctgttctg 1740
tgttaccac atccccacac ccatttgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttgaaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1                      5                      10                      15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20                      25                      30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35                      40                      45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50                      55                      60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                                  360                                  365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
           370                                  375                                  380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                                  390                                  395                                  400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tctccaggg 60  
 cagcaccatg cagcccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcattccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcattggagc agcggtgccc gcccacagc gagctggtgc aggcctgctt 420  
 gcggtcttcc caggagccgg tccccaggc cgcgtgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cggggccggg tgaccgtcga gtggtgccc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggctggg gtccgtccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggcctgga acttctggca gcagctgagc cggccccggc agccgctgct 660  
 gctacaggtg tcggtgcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720  
 ggtccgcttt gctcgcagc gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gaggcctgg ccttcaagtg gccgtttctg gggcctcgac agtgcacgc 1020  
 ctcgagact gactcgctgc ccatgatcgt cagcatcaag gaggaggcca ggaccaggcc 1080  
 ccagggtggtc agcctgcccc acatgagggg gcagaagtgc agctgtgcct cggatggtgc 1140  
 gctcgtgccca aggaggtccc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttctctgac aagttacctc 1320  
 acctaatatt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380  
 ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtccctc accaccactc tggacctaag acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45



Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115  
 aggactgccca taacttgcct g 21

<210> 116  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116  
 ataggagtgtg aagcagcgct gc 22

<210> 117  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117  
 tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118  
 <211> 1857  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
 gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcttgagaat 180

```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaa 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
tacacctggg tcaaagatgg gatagtgat cctacgaatc ccaaaagcac cgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcatgga agctgtggag cggaatgtgg gggtcacgtg ggcagccgtc 780
cttgtaaccc tgattctcct ggggaatcttg gtttttggca tctgggttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tccagtaaga aggtgattta cagccagcct 900
agtgccgaa gtgaaggaga attcaaacag acctcgctcat tcctgggtgtg agcctgggtcg 960
gctcaccgcc tatcatctgc atttgcctta ctccaggtgt accggactct ggccccctgat 1020
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcacgc cctccctccc 1140
tttctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200
agggatcagg aaggaatcct ggggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
tgggcggggg cgcaggaaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggcagctgt 1380
tctagagcgg gaattagagg cttagagcggc tgaaatgggt gtttgggtgat gacactgggg 1440
tccttccatc tctggggccc actctcttct gtcttcccat ggggaagtgcc actgggatcc 1500
ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttggt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggatttaaa 1620
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcggg tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1              5              10              15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20              25              30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35              40              45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50              55              60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65              70              75              80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85              90              95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tgcggagct gtgttctgtt tccc

<210> 121

<211> 50

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctgggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 125

actcagcagt ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

```

cagcgcgtgg cggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccgactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gtcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300
ggattgagcc atgtacccag aaagggcaat gccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgtgcga cggccacca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tgggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctccctcttt 780
tgtcctggct ccgagcccag gagcgccctc gccactggg gttactggtg gccatgaagg 840
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaaccgcagc 1020
tcctgcagaa gtggccctgg agattgaggg tcctgggaca ctccctatgg agatccgggg 1080
agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc                                     1210

```

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

```

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1                      5                      10                      15

```

```

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
      20                      25                      30

```

```

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
      35                      40                      45

```

```

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
      50                      55                      60

```

```

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
      65                      70                      75                      80

```

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                             85                            90                            95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                             100                            105                            110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                             115                            120                            125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                             130                            135                            140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                             145                            150                            155                            160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                             165                            170                            175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                             180                            185                            190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                             195                            200                            205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                             210                            215                            220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala  
                             225                            230                            235                            240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                             245                            250                            255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                             260                            265                            270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                             275                            280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130

gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc

50

<210> 131

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1837)

<223> a, t, c or g

<400> 131

```

cccacgcgtc cggctctcgct cgctcgcgca gcggcggcag cagaggctgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gagggaaagga agctgcatgc atgagaccca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccaga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcgccct gcacagctca 300
cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaaggcgctt acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatac 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
atgaaggatt caagatccgg taccgccgac tacacaatat gggttcatta tgcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggtatgtt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt gagtcacgga gatttcgtct gccacccgag gccttgtagc cgctacaacc 960
acggaactgt ggtggagttt tactgcgacg ctggctacag cctcaccagc gactacaagt 1020
acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatac 1080
agcaaactgt gccagcacc catgagaccc tctgaccac gtggaagatt gtggcggttca 1140

```



```
<210> 132
<211> 490
<212> PRT
<213> Homo sapiens
```

<400> 132															
Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1				5					10					15	
Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
			20					25					30		
Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
		35					40					45			
Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
	50					55				60					
Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65					70					75					80
Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
				85					90					95	
Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
			100					105					110		
Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
		115					120					125			
Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
	130					135					140				
Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145					150					155					160
Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
				165					170					175	
Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn

[illegible]

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgctg cggtcgcgtc gtggcctaga 60  
gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120  
ccgtagegcc cgagtgtcgg ggggcgcacc cgagtcggggc catgaggccg ggaaccgcgc 180  
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240  
tgagtgcctc ggatttggac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300

```

ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagtcc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatthagga actgggtatgt ggatgagccg tcctgcggca 600
gcgaggctctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccctt 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaattatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900
ttgtgggtcac cacagttgta tgttggggtt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagacc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200
tgagcgtgga gagtgattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgtttgg acccccacgt tttggctgta tcctttatcc cagccagtc 1500
tccagctcga cttatgaga aggtacctg ccagggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<210> 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtaactg 240  
 cctgcaccag cggcgggtgg cctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggg gcaggtcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtgggc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcggtc 660  
 cactaacatt tttcggaatc tggagtccac ccgttggttg ctggctgggc ttttccagtg 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatcc 780
caactaccaa agctgctgga gectgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcactctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga gggtgccttg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1             5             10             15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20             25             30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35             40             45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50             55             60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65             70             75             80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85             90             95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100            105            110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115            120            125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130            135            140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145            150            155            160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165            170            175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence



<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 143  
 ccaactacca aagctgctgg agcc 24

<210> 144  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 144  
 gcagctctat taccacggga agga 24

<210> 145  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 145  
 tccttcccgt ggtaatagag ctgc 24

<210> 146  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 146  
 ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147  
 <211> 1686  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 ctctctttaa catacttgca gctaaaacta aatattgctg cttggggacc tcctttctagc 60  
 cttaaatttc agtcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
 ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

```

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtatatt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
gagctctttc tccccagtc cagaggggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccgggcc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900
ctgtgatgac aactggggag aaaaggagga ccagggtgga tgcaagcaac tgggctgtgg 960
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccttggg ttggccgcat 1020
ctggctggat aatgttcgtt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080
atattggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140
ggtgggcatc atctaactg ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200
atttactgtc tacatgactg catgggatga acactgatct tcttctgccc ttggactggg 1260
acttatactt ggtgcccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320
aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380
tccacattgc acacagcaga tcccagcct ccataattgt gtgtatcaac tacttaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgtttctctg aagaactctg acaaaataca gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaaact tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

```

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgacactcg 60
accacgcgt ccgcggacgc gtggcgccg gcgtgggccg gctaccagga agagtctgcc 120
gaaggatgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
cctgggcgctc ttccggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
gaatgctgtg gtggtgatca caggcgccac ctcagggtct ggcaaagaat gtgcaaaagt 300
cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
ggtgaccttc gacctcacag actctggggc catagtgtgca gcagcagctg agatcctgca 480
gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcacccg 840
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
cttactgcct tccttggtctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttggttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttggccgcc atggccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1             5             10             15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20             25             30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
          35             40             45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
          50             55             60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
          65             70             75             80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85             90             95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
          100            105            110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
          115            120            125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
          130            135            140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
          145            150            155            160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165            170            175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
          180            185            190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
          195            200            205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	295 300
Arg Lys Ser Lys Asn Ser		
305	310	

&lt;210&gt; 154

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 154

ggtgctaaac tggctgctctg tggc

24

&lt;210&gt; 155

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 155

cagggcaaga tgagcattcc

20

&lt;210&gt; 156

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156  
tcataactgtt ccatactcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtgggtaaaa 60  
aaaaaaaaaa acacaccaaaa cgctcgcagc caaaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattggggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggaactgg gtgccaaggt 360  
tcataacctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatatt agtaaataat gctgggtgtag tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg ctactgttc 660  
aagcaagttt gctgctgttg gatctcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaacaa catgtctgtg tctaatttc gttaaactg gcttcatcaa 780  
aaatccaagt acaagtttgg gaccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccatttct tcaatatcat ttttgaggct ttggcagctc 1140  
tcatttacta ccacttggtc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaatgac tttattaaaa 1260  
taatttcaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320  
ttatttaaca tatattttta tttttgattg cacttaaatt ttgtataatt tgtgtttctt 1380  
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
tagtggattt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500  
gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagaggty gatacacgtg ttgcaagta aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta ccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1771

<210> 159

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val  
 1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
 20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
 35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
 50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
 100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
 245 250 255



Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
                   260                                  265                                  270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
                   275                                  280                                  285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
                   290                                  295                                  300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

```

attgttttcgc tggctcctggt gatgcctggc cctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttaca cagcaacctc 360
ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
caggggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcctttgaa 960
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080
tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140
tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200
ccatggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260
atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320
caggaataca agaaggcaga aaaaaaagtt tggaagatct ttaaactctga cagtgaagtg 1380
gctgggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
attttacct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500
aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620
tcatatctgc aagatTTTTT tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
TTTTGGGGGG agatgtttac taaaaatta acatgagtac atgagtaaga attacattat 1740
ttaaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
TTTTAGGGTC ttgaatagga agttttaatt tcttctaaga gtaagtgaag agtgcagttg 1860
taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920
gtgttttgaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

```

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

```

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
  1                      5                      10                     15

```

```

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
      20                      25                     30

```

```

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
      35                      40                     45

```

```

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
      50                      55                     60

```

```

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```

65					70					75				80	
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150				155						160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225				230						235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245				250						255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260				265						270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165

ttccatgccca cctaaggagg actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctggtcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggcttt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60  
 atttttcctt ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120  
 tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180  
 tccttgcttc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtggagt 240  
 gatggaagtc taaaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300  
 cctggagagc ctgggggagg gcctgcctaa caagctttca aaaaacagga gcgacttcca 360  
 ctgggctggg ataagacgtg ccggtaggat aggggaagact gggtttagtc ctaatatcaa 420  
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480  
 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540  
 tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600  
 gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
 accaggatgg ggaccctggg tcaggccagc ctctttgtct ctcgccgaaa ttatttttgg 720  
 tctgaccact ctgccttgtg ttttgacaga tcatgtgagg gccaaaccggg gaaggtggag 780  
 cagatgagca cacacaggag ccgtctctct accgcgcgcc ctctcagcat ggaacagagg 840  
 cagccctggc cccgggccct ggaggtggac agccgctctg tggctctgct ctcagtggctc 900  
 tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960  
 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020  
 ggggccatca accgggtcta taagctgaca ggcaacctga ccatccaggt ggctcataag 1080  
 acagggccag aagaggacaa caagtctcgt taccgcgcgc tcactcgtgca gccctgcagc 1140  
 gaagtgtcga ccctcaccaa caatgtcaac aagctgtcga tcattgacta ctctgagaac 1200  
 cgctgctgg cctgtgggag cctctaccag ggggtctgca agctgctgcg gctggatgac 1260  
 ctcttcaccc tgggtggagcc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320  
 acgggcacca tgtacggggg gattgtgcgc tctgaggggtg aggatggcaa gctcttcac 1380  
 ggacggctg tggatgggaa gcaggattac ttcccgacc tgtccagccg gaagctgccc 1440  
 cgagaccctg agtcctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500  
 ctcatcaaga tcccttcaga caccctggcc ctgggtctccc actttgacat cttctacatc 1560  
 tacggctttg ctagtggggg ctttgtctac tttctcactg tccagcccga gacccttag 1620  
 ggtgtggcca tcaactccgc tggagacctc ttctacacct caagcatcgt gcggctctgc 1680

```
<210> 170
<211> 552
<212> PRT
<213> Homo sapiens
```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr  
1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctcccc gcgaggctga gtgcggactg gagggggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctgggtccctc 180  
tgcggtcccg ccacgcacag ctggggctgc agggccaaggg ctgggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgctg ccaggccctc 480  
acatctgcag tgagatggac ctgggggctg tggccagctg gctactccaa gaccctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat tttgaccacc 600  
tgatgtccag ggtggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgcca ccatcaactt gcagtcaaca cagagctgc 840  
agctactgac cacctttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900  
actggacggg gtggtttgac tcgtggggag gccctcaca tatcttgat tcttctgagg 960  
ttttgaaaac cgtgtctgac attgtggagc ccggctcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcataaatg gagccatgca ctcccatgac tacaagtac 1080  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttgggtcca tctcaggcat cctctccct ccccccactg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
acgccctcaa gtacctggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320  
tgccagtcaa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380  
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcagggtgtt gtgaacacag 1440  
tatccatagg attcttgagc tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaaat 1680  
gngtccctt cccagaaaca cccacattac ctgctttctt cttgggtagc ttgtccatca 1740  
gtccacgcc ttgtgacacc tttctgaagc tggagggtct ggagaagggg gttgtattca 1800  
tcaatggcca gaaccttgga cgttactgga acattggacc ccagaagacg ctttacctcc 1860  
caggctccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920  
gccctgcatt acagttcacg gaaaccccc accctggcag gaaccagtac attaatgag 1980  
cgggtggcacc cctcctgctc ggtgccagt ggagactgcc gcctcctctt gacctgaagc 2040  
ctgggtggctg ctgccccacc cctcactgca aaagcatctc ctttaagtagc aacctcaggg 2100  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg 2160  
ggatggctct gggcctggct ttgttgatga tggttttct acagccctgc tcttgtgcgg 2220  
aggctgtcgg gctgtctcta ggggtgggag agctaatac atcgcccagc ctttggccct 2280

```

cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcatctgctg 2340
gactcaggcg tgctctttgc tggttcctgg gaggcttggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttccccctt tcccttccca ctcgctgctt cccacaggg 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcaggtgt 2640
ctctgggtgt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggccagct 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaaagta taaccttgaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1                      5                      10                      15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20                      25                      30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
          35                      40                      45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
  50                      55                      60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
  65                      70                      75                      80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85                      90                      95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
          100                     105                     110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
          115                     120                     125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
          130                     135                     140

```

Leu 145	Gly	Gly	Leu	Pro	Ser 150	Trp	Leu	Leu	Gln	Asp 155	Pro	Gly	Met	Arg	Leu 160
Arg	Thr	Thr	Tyr	Lys 165	Gly	Phe	Thr	Glu	Ala	Val	Asp	Leu	Tyr	Phe	Asp 175
His	Leu	Met	Ser 180	Arg	Val	Val	Pro	Leu 185	Gln	Tyr	Lys	Arg	Gly	Gly	Pro 190
Ile	Ile	Ala 195	Val	Gln	Val	Glu	Asn 200	Glu	Tyr	Gly	Ser	Tyr 205	Asn	Lys	Asp 210
Pro	Ala 210	Tyr	Met	Pro	Tyr	Val 215	Lys	Lys	Ala	Leu	Glu 220	Asp	Arg	Gly	Ile 225
Val 225	Glu	Leu	Leu	Leu	Thr 230	Ser	Asp	Asn	Lys	Asp 235	Gly	Leu	Ser	Lys	Gly 240
Ile	Val	Gln	Gly	Val 245	Leu	Ala	Thr	Ile	Asn 250	Leu	Gln	Ser	Thr	His	Glu 255
Leu	Gln	Leu	Leu 260	Thr	Thr	Phe	Leu	Phe 265	Asn	Val	Gln	Gly	Thr 270	Gln	Pro 275
Lys	Met 275	Val	Met	Glu	Tyr	Trp	Thr 280	Gly	Trp	Phe	Asp	Ser 285	Trp	Gly	Gly 290
Pro 290	His	Asn	Ile	Leu	Asp	Ser 295	Ser	Glu	Val	Leu	Lys 300	Thr	Val	Ser	Ala 305
Ile 305	Val	Asp	Ala	Gly	Ser 310	Ser	Ile	Asn	Leu	Tyr 315	Met	Phe	His	Gly	Gly 320
Thr	Asn	Phe	Gly	Phe 325	Met	Asn	Gly	Ala	Met 330	His	Phe	His	Asp	Tyr 335	Lys 340
Ser	Asp	Val	Thr 340	Ser	Tyr	Asp	Tyr	Asp 345	Ala	Val	Leu	Thr	Glu 350	Ala	Gly 355
Asp	Tyr 355	Thr	Ala	Lys	Tyr	Met	Lys 360	Leu	Arg	Asp	Phe	Phe 365	Gly	Ser	Ile 370
Ser 370	Gly	Ile	Pro	Leu	Pro	Pro 375	Pro	Pro	Asp	Leu	Leu 380	Pro	Lys	Met	Pro 385
Tyr 385	Glu	Pro	Leu	Thr	Pro 390	Val	Leu	Tyr	Leu	Ser 395	Leu	Trp	Asp	Ala	Leu 400
Lys	Tyr	Leu	Gly	Glu 405	Pro	Ile	Lys	Ser	Glu 410	Lys	Pro	Ile	Asn	Met	Glu 415
Asn	Leu	Pro	Val 420	Asn	Gly	Gly	Asn 425	Gly	Gln	Ser	Phe	Gly	Tyr 430	Ile	Leu 435

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

```

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60
ccctggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggcccaggg ccccaggac ctccatctcc caatgttgga 180
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaaccgcca 240
tggtcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360
tagacggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

```

```

tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttgggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720
aggtcttgct gcccaagata tatccatggc tttatcacia tgggggcaac atcattagca 780
ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840
tggctgggct cttccgtgca ctgctaggag aaaagatcct gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
ctgacaacat gaccaaaatc tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020
taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggt 1080
ctgtgtcagc tgtaaccaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtgccat aagaaggac 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatactctgaa gcaggggacc 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttccttttg 1320
gacctttacc tcccccgagc cccaagatga tgcttggacc tgtgactctg cactgggttg 1380
ggcatttact ggctttccta gacttgcttt gcccccgtgg gccattcat tcaatcttgc 1440
caatgacctt tgaggctgtc aagcaggacc atgggttcat gttgtaccga acctatatga 1500
cccataccat ttttagccca acaccattct ggggtccaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620
tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680
tcagcttttg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800
ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980
ggccacaaca gaccctctac gtgccaagat tcctgctgtt tcctagggga gccctcaaca 2040
aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
atacactgag tgccctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
ggtggctcat gctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagtga tggagggtgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaaa 2505

```

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

```

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1                      5                      10                      15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
          20                      25                      30

```

```

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
  35                      40                      45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
  50                      55                      60

```

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	400
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
	405	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
	420	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
	435	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
	450	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	480
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
	485	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
	500	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
	515	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
	530	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	560
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
	565	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
	580	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
	595	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gcc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22



<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttaoctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagtgt agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300  
 ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cggccaggac aagcaggagt 420  
 tgcatctgtt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagtccctt ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctttaagaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaaactg atttaaaagt caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattaccc atgtcaaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcagatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaaag tggacattct gccaaaacaa ttgtttaaat 1320

```

gcataaaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500
tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
ttgcaaattg gatTTaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
ctttttaaataaaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta gggTTTTaag tcattcattt ccaaattcatt tttttttttc ttttggggaa 1800
agggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgcctgctaa agtaaattgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaa 1947

```

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1              5              10              15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20              25              30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35              40              45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50              55              60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65              70              75              80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
      85              90              95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
      100              105              110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
      115              120              125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
      130              135              140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
      145              150              155              160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
      165              170              175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
      180              185              190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465                                      470                                      475                                      480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro

                                    485                                      490                                      495

Phe Ala Asn Gly Ile

                                    500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c 21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg 24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctega atccttacca gtggcag 47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60  
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120  
 aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctcccttg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
 gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300  
 atcgttggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtcctttac 360  
 ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420  
 cacaaccag acaaggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480  
 tcttgctctg ccttgcaagt ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
 ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
 cagctgctgg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780  
 ggggagagag aaccctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tcggtcctta aggctgcccc gcgccttgcc 960  
 aaaatggagc ttgtaagaag gctcatgcc a ttgacctct taattctctc ctgtttggcg 1020  
 gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct agggggtgcc 1080  
 aatatggcag agaccacaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
 tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttcta tgtccagctt 1200  
 gatccagatg gaagctgtga aagtgaaac attaaagtct ttgacggaac ctccagcaat 1260  
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttcctgtatt tgaatcatca 1320  
 tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
 gtcttctact acttcttctc tctaacatc tctattccaa actgtggcgg ttacctggat 1440  
 accttggag gatccttcac cagccccaat tacccaaagc cgcctcctga gctggcttat 1500  
 tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
 ttctagaaa tagacaaaca gtgcaaat t gattttcttg ccatctatga tggccctctc 1620  
 accaactctg gctgattgg acaagtctgt ggcctgtgta ctcccacct cgaatcgtca 1680  
 tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
 gcttcttaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800  
 gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc taatgggaat 1860  
 aacttgcaac taaaagacct aacttgcaag ccaaaattat caaatgttgt ggaattttct 1920  
 gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
 aatataatca ccttttctgc atcctcaact tctgaagtga tcaccctca gaaacaactc 2040  
 cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
 gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataaccag catggctctt 2160  
 tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
 caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280  
 gatacctgta gagcctctcc cacctctgac tttgcatctc caacctacga cctaatacag 2340  
 agtggatgta gtgcagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400  
 ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
 gttttgatat gtgatagcag tgaccaccag tctcgtgca atcaagggtg tgtctccaga 2520  
 agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580  
 ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640  
 gaaactccaa accagccttt caacagtgtg catctgtttt ccttcattgg tctagctctg 2700  
 aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met	Glu	Leu	Val	Arg	Arg	Leu	Met	Pro	Leu	Thr	Leu	Leu	Ile	Leu	Ser	1	5	10	15
Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys	20	25	30	
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met	35	40	45	
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg	50	55	60	
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp	65	70	75	80
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr	85	90	95	
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr	100	105	110	
Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val	115	120	125	
Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	130	135	140	
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	145	150	155	160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu	165	170	175	
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile	180	185	190	
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys	195	200	205	
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu	210	215	220	
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser	225	230	235	240
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg	245	250	255	
Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr	260	265	270	
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys	275	280	285	

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
		580						585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
		595					600					605			

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120  
 ctgctgctgc cgccgccgcc gtgccctgcc cacagcgcca cgcgcttcga cccacactgg 180



```

gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
atccactggg gagtgttttc cgtgcccagc ttcggtagcg agtggttctg gtggatttgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtttc 360
aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420
gatatttttc aggcctcttg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccagg 540
agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttggg 600
ctgtactatt ccttttttga atggtttcat ccgctcttcc ttgaggatga atccagtcca 660
ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840
accaatgata gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960
aaactgtcct ggggctatag gaggaagct ggaatctctg actatcttac aattgaagaa 1020
ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaatattggg 1080
cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtggggtcc 1140
tggctaaaaa tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200
actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260
tttcttaaat ggcccacatc aggacagctg ttccttggcc atcccaaagc tattctgggg 1320
gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380
aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
tggtgctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500
atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620
ttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680
cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattgggtg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800
tatatagtta tgcatcactt aatatgggga tattttctgg gaaatgcatt gctagtcaat 1860
ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacaccta atgtgatggt tagactgttg ctccctaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040
gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagtgtctc tgggtgagtc agtgagtga tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aattttttaa accttttttg ctcttttgta ataacactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa
2362

```

&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

```

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
  1              5              10              15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
          20              25              30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
  35              40              45

```

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe		
	50						55				60						
Ser	Val	Pro	Ser	Phe	Gly	Ser	Glu	Trp	Phe	Trp	Trp	Tyr	Trp	Gln	Lys		
	65				70					75					80		
Glu	Lys	Ile	Pro	Lys	Tyr	Val	Glu	Phe	Met	Lys	Asp	Asn	Tyr	Pro	Pro		
				85					90					95			
Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe		
			100					105					110				
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr		
		115					120					125					
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser		
	130					135					140						
Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp		
	145				150					155					160		
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg		
				165					170					175			
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu		
			180					185					190				
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys		
		195					200					205					
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val		
	210					215					220						
Leu	Trp	Ser	Asp	Gly	Asp	Gly	Gly	Ala	Pro	Asp	Gln	Tyr	Trp	Asn	Ser		
	225				230					235					240		
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr		
				245					250					255			
Val	Val	Thr	Asn	Asp	Arg	Trp	Gly	Ala	Gly	Ser	Ile	Cys	Lys	His	Gly		
			260					265					270				
Gly	Phe	Tyr	Thr	Cys	Ser	Asp	Arg	Tyr	Asn	Pro	Gly	His	Leu	Leu	Pro		
		275					280					285					
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr		
	290					295					300						
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val		
	305				310					315					320		
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn		
				325					330					335			

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
                   340                  345                  350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
                   355                  360                  365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
                   370                  375                  380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
                   385                  390                  395                  400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
                   405                  410                  415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
                   420                  425                  430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
                   435                  440                  445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
                   450                  455                  460

Asn Val Ile  
                   465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgcgagc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcagggaaa tccggatgtc tccggttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gactagtatt tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcaacttccat ctggaccacg aggtctcctgg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccagggt gtcatgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtggtcatc tctaggatta gcccaaacc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaa gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tctctctgct 720  
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttgttg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctctcttc 900  
 tttggtgctg cagctggtct tggattttgc tatgtcaaaa ggtatgtgaa ggcttccct 960  
 tttacaaaaca agaatcagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaatca aagaaaaactg ataaaaacc agaagatcc 1080  
 aagagtccaa gcaaaactac cgtgcatgct ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggt tggtttcttt catgctcctt accctgcccc agctggggaa 1200  
 atcaaaaggg ccaaagaacc aaagaagaaa gtccaccctt ggttcttaac tggaaatcagc 1260  
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320  
 cctgtctgga tcctatctc ctacctcaa agcttccac gccctttcta gctggctat 1380  
 gtcctaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```

tcattcagtat ccagtggtaa aaaggcctcc tggctgtctg aggetaggtg ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga caggggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgtttag aacacacaca cttacttttt ctgggtctcta ccactgctga tttttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
ttttttcagt tttgatattt ctagcttatt tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca ctttttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1              5              10              15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
          20              25              30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
          35              40              45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
          50              55              60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
          65              70              75              80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
          85              90              95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
          100             105             110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
          115             120             125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
          130             135             140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 203  
 gtcagtgcaca gtacctactc gg 22  
  
 <210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 204  
 tggagcagga ggagtagtag tagg 24  
  
 <210> 205  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 205  
 aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50  
  
 <210> 206  
 <211> 1620  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> modified\_base  
 <222> (973)  
 <223> a, t, c or g  
  
 <220>  
 <221> modified\_base  
 <222> (977)  
 <223> a, t, c or g  
  
 <220>  
 <221> modified\_base  
 <222> (996)  
 <223> a, t, c or g  
  
 <220>  
 <221> modified\_base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggt cttggcacct ctaattgtct tctgttattc ggtgcccga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgtcttc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggt aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttggata ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggtc acttggattg 480
tggagtctct tgccaattgg tctaataact gccaatcatt tgccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcgttac aaagttagca catcacccct caccaagcaa ctccctaccc 660
tgatcctggt ccaaggtggc aaggaggcaa tgcggcggcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gacgagcctg 840
tggcttcaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctc cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcacc ctaggaagg cctgccatgc 1080
tgtggccaac tgtttactg gagcaagaaa gagatctcat aggacggagg gggaaatggt 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tcttcttag ttgacctgca cagcttggtt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccttaa gcccttctgg ctctgtttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggttgag 1500
actttccttt gtgtggtagg acttgaggga gaaatccctt ggactttcac taacctctg 1560
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttcctttt 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1                      5                      10                      15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20                      25                      30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35                      40                      45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50                      55                      60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65                      70                      75                      80

```



Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

gcttgatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggcccccca gagctctagc cgctcaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcttgccccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
 cccattgctc ctgctgcccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggtcattgg aaagacctcc ttaatggagt 240  
 gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccctgc cgctaccgct acgagccggc cctggtctcc ccgcggcggtg tgcgtgtcaa 360  
 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420  
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcggt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600

```

ctttccttac cagtccccca acgggcgcta ccagttcaac ttccaagagg gccagcaggt 660
ctgtgcagag caggctgcgg tgggtggcctc ctttgagcag ctcttccggg cctgggagga 720
gggcctggac tgggtgcaacg cgggctggct gcaggatgct acggtgcagt accccatcat 780
gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcggtgcgaa gctacggccc 840
ccgccaccgc cgctgcacc gctatgatgt attctgcttc gctactgcc tcaaggggcg 900
ggtgtactac ctggagcacc ctgagaagct gacgtgaca gaggcaaggg aggcctgcca 960
ggaagatgat gccacgatcg ccaaggtggg acagctcttt gccgcctgga agttccatgg 1020
cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080
cccgcaccc cactgtgggc cccagagacc tgggggccga agctttgggt tccccgacct 1140
gcagagccgc ttgtacggtg ttacttgcta ccgccagcac taggacctgg ggccctcccc 1200
tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260
agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacad tttttacta 1320
ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380
aatcatgctt gctccccctg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440
atccaggctg gtctccctcc ctttaaggagg ttggtgcccc gagtgggagg tggcctgtct 1500
agaatgccgc cgggagtcgg ggcagtggtg gcacagttct cctgccccct cagcctgggg 1560
gaagaagagg gcctcggggg cctccggagc tgggcttttg gcctctcctg cccacctcta 1620
cttctctgtg aagccgctga cccagtcctg cccactgagg ggctaggggt ggaagccagt 1680
tctaggcttc caggcgaaat ctgagggaag gaagaaaact cccctccccg tccccctccc 1740
ctctcggttc caaagaatct gttttgttgt catttgtttc tcctgtttcc ctgtgtgggg 1800
aggggcccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaa                                             1985

```

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

```

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1                      5                      10          15

```

```

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
      20                      25          30

```

```

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
      35                      40          45

```

```

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
      50                      55          60

```

```

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
      65                      70          75          80

```

```

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
      85                      90          95

```

```

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
      100                     105          110

```

```

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

115					120					125								
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr			
130					135					140								
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu			
145					150					155					160			
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg			
					165					170					175			
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala			
					180					185					190			
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly			
					195					200					205			
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr			
					210					215					220			
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro			
					225					230					235		240	
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp			
					245					250					255			
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu			
					260					265					270			
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu			
					275					280					285			
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys			
					290					295					300			
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser			
					305					310					315		320	
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu			
					325					330					335			
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr			
					340					345					350			
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His											
					355					360								

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttggtg ggttgag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagtgag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ggagagcggg gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60  
 gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120  
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180  
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgcgggggac ggcgacggct ggggtgtcgt ggcgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcgtgag cgcggcctgg gacacgtao acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctcgc caacgccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
 gcggcgtttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttctct caccgcgagg agttccctca catgcgggac atcgtgattg ctgaaacctt 660  
 ggaggacctg gacagaaaca aagatggcta tgtccaggtg gaggagtaca tcgcggatct 720  
 gtactcagcc gacctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840  
 ggtgctgccc cctgcccagg accagcccct ggtggaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020  
 agcaccgcgc acctgccaca gcctcagagg ccgcacaaat gaccggagga ggggcgctg 1080  
 tggcttgccc cctccctgt ccaggcccc caggaggcag atgcagtccc aggcatactc 1140  
 ctgcccctgg gctctcaggg accccctggg tcggcttctg tccctgtcac accccaacc 1200  
 ccaggaggagg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260  
 cagcccagac ccagggaccc ttggcccca gctcagctct aagaaccgcc ccaaccctc 1320  
 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380  
 tgcttgccct ggctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



&lt;400&gt; 225

ccccctgag cgacgctccc ccatgatgac gccacggga actt

44

&lt;210&gt; 226

&lt;211&gt; 2403

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 226

```

ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt ggggagcccc 60
gggcggcggg cgccgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgtct 120
ccagcctgtc tgtcgtcgtt ttggcgcccc cgccctcccc cggtgcgggg ttgcacaccg 180
atcctgggct tcgctcgatt tgccgcgag ggcctccca gacctagagg ggcgtggcc 240
tggagcagcg ggtcgtctgt gtctctctc ctctgcgcg cgcgcgggga tccgaagggt 300
gccccggctc gaggaggtga cgcgcggggc ctcccgacc ctggccttgc ccgcattctc 360
cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggtc 420
tcggcctcgg tgtgtgtctg ctgctgtctc cggggcccg gggcagcgag ggagccgctc 480
ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540
tctgcccagg gggctgcctt cttgaggaat tctctgtgta tgggaacata gtatatgctt 600
ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660
ctgtacgagt ctatagccta cctggctcag aaaactattc ctcagtagat gccaatggca 720
tccagtctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaagta 780
gtacacagga ggccacagga caagcagtg ccacagcaca tccaccaaca ggtaaacgac 840
taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900
tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960
gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020
ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080
tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140
agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atcccccagg 1200
tggttggtgt atttattgat ggttggcctt ctgatgacat cgaggaagca ggcattgtgg 1260
ccagagagtt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320
tggggatggt tcaggatgtc acatttgttg acaaggctgt ctgtcggaat aatggcttct 1380
tctcttacca catgcccac tggtttggca ccacaaaata cgtaaagcct ctggtacaga 1440
agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500
ccttttctaat tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560
ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620
tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680
atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggaacagct actggtgatg 1740
ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800
tcctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860
cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920
tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gagtccacag 1980
gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100
attgtattct cataacttg aaatgcttta gcatactaga atcagataca aaactattaa 2160
gtatgtcaac agccatttag gcaataaagc actcctttaa agccgctgcc tcttggttac 2220
aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataatactgg ctcttagaaa 2280
ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340
tgtacagata tgcaaattcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaaa 2400
aaa
2403

```

&lt;210&gt; 227

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

```

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
  1           5           10           15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
          20           25           30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
          35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
          50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
          65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
          85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
          100          105          110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
          115          120          125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
          130          135          140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
          145          150          155          160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
          165          170          175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
          180          185          190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
          195          200          205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
          210          215          220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
          225          230          235          240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
          245          250          255

```

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
tggtctcgca caccgatc 18

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229  
ctgctgtcca caggggag 18

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
ccttgaagca tactgctc 18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa tttccgcc 18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233

cttggcacca atgtccgaga tttc

24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234

gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

```

cgccgcgctc ccgcacccgc ggcccgcgcc ccgcgcgct cccgcctctg caccgcgagc 60
ccggcgggct cccggcgggg gcgagcagat ccagtccggc ccgcagcgca actcgggtcca 120
gtcggggcgg cggtgcggg gcgagagcgg agatgcagcg gcttggggcc accctgctgt 180
gcttgcctgt ggcggcgggc gtccccacgg ccccgcgcc cgctccgacg gcgacctcgg 240
ctccagtcga gcccggcccc gctctcagct accgcagga ggaggccacc ctcaatgaga 300
tgttccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360
aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420
tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480
atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540
agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcgc 600
acgaggactg tggggccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660
catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

```

```

gtgtctgggg tcactgcacc aaaatggcca ccaggggcag caatgggaacc atctgtgaca 780
accagagggga ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccctg 840
tgtgcacacc cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttcttg 900
acctcatcac ctgggagcta gagcctgatg gagccttgga ccgatgccct tgtgccagtg 960
gcctcctctg ccagccccac agccacagcc tgggtgatgt gtgcaagccg accttcgtgg 1020
ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtccccgat gagtatgaag 1080
ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140
aagagatggc gctgggggag cctgcggctg ccgcccgtgc actgctggga ggggaagaga 1200
tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt tatttcccca 1260
gggtgtgtgct ttaggcgtgg gctgaccagg cttcttccta catcttcttc ccagtaagtt 1320
tcccctctgg cttgacagca tgaggtgttg tgcatttggt cagctcccccc aggctgttct 1380
ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaaactgca ggagcagttt 1440
gccacccctg tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt 1500
tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560
tgattggttt tggggaaatg tggagaagag tgccctgctt tgcaaaccatc aacctggcaa 1620
aaatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680
cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740
gtgttgctca gctcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc 1800
tctctcagca cagcctgggg aggggggtcat tgttctcctc gtccatcagg gatctcagag 1860
gctcagagac tgcaagctgc ttgccaagt cacacagcta gtgaagacca gagcagtttc 1920
atctggttgt gactctaagc tcagtgtctt ctccactacc ccacaccagc cttggtgcca 1980
ccaaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040
attaaggtca aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160
ctttggcagt tgcattagta actttgaaag gtatatgact gagcgtagca tacagggttaa 2220
cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280
cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340
tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460
taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520
aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
aaaaaa

```

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

```

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
  1                      5                      10                      15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
                20                      25                      30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
    35                      40                      45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50                      55                      60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
    65                      70                      75                      80

```

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
                             85                            90                            95  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                             100                            105                            110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                             115                            120                            125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                             130                            135                            140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                             145                            150                            155                            160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                             165                            170                            175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                             180                            185                            190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                             195                            200                            205  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
                             210                            215                            220  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                             225                            230                            235                            240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                             245                            250                            255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
                             260                            265                            270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
                             275                            280                            285  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
                             290                            295                            300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
                             305                            310                            315                            320  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
                             325                            330                            335  
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
                             340                            345                            350

&lt;210&gt; 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 237  
 ggagctgcac cccttg 17  
  
 <210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
 ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 239  
 gcagagcgga gatgcagcgg ctg 24  
  
 <210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 240  
 ttggcagctt catggagg 18  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 241  
 cctgggcaaa aatgcaac 18



<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc 24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg 45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50  
 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacatata 150  
 cacacatata ccttctcttc cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcctggcc 250  
 attacctctg cagctccttt ggcttggtga gtcaaaaaaac atgggagggg 300  
 ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350  
 tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

ggggtagata	ctgcttctct	gcaacctcct	taactctgca	tcctcttctt	650
ccagggctgc	ccctgatggg	gcctggcaat	gactgagcag	gccagcccc	700
agaggacaag	gaagagaagg	catattgagg	agggcaagaa	gtgacgcccc	750
gtgtagaatg	actgccctgg	gagggtggtt	ccttgggccc	tggcaggggt	800
gctgaccctt	accctgcaaa	acacaaagag	caggactcca	gactctcctt	850
gtgaatggtc	ccctgccctg	cagctccacc	atgaggcttc	tcgtggcccc	900
actcttgcta	gcttgggtgg	ctggtgccac	tgccactgtg	cccgtggtac	950
cctggcatgt	tcctgcccc	cctcagtgtg	cctgccagat	ccggccctgg	1000
tatacgcccc	gctcgtccta	ccgcgaggct	accactgtgg	actgcaatga	1050
cctattcctg	acggcagtcc	ccccggcact	ccccgcaggc	acacagaccc	1100
tgctcctgca	gagcaacagc	attgtccgtg	tggaccagag	tgagctgggc	1150
tacctggcca	atctcacaga	gctggacctg	tcccagaaca	gcttttcgga	1200
tgcccgagac	tgtgatttcc	atgccctgcc	ccagctgctg	agcctgcacc	1250
tagaggagaa	ccagctgacc	cggctggagg	accacagctt	tgcagggctg	1300
gccagcctac	aggaactcta	tctcaaccac	aaccagctct	accgcatcgc	1350
ccccagggcc	ttttctggcc	tcagcaactt	gctgcggctg	cacctcaact	1400
ccaacctcct	gagggccatt	gacagccgct	ggtttgaaat	gctgccccaac	1450
ttggagatac	tcatgattgg	cggcaacaag	gtagatgcca	tcctggacat	1500
gaacttcctg	cccttgcca	acctgcgtag	cctggtgcta	gcaggcatga	1550
acctgcggga	gatctccgac	tatgccctgg	aggggtgca	aagcctggag	1600
agcctctcct	tctatgacaa	ccagctggcc	cgggtgcccc	ggcgggcact	1650
ggaacaggtg	cccgggctca	agttcctaga	cctcaacaag	aaccgcctcc	1700
agcgggtagg	gccgggggac	tttgccaaca	tgctgcacct	taaggagctg	1750
ggactgaaca	acatggagga	gctggtctcc	atcgacaagt	ttgccctggt	1800
gaacctcccc	gagctgacca	agctggacat	caccaataac	ccacggctgt	1850
ccttcatcca	ccccgcgcc	ttccaccacc	tgccccagat	ggagaccctc	1900
atgctcaaca	acaacgctct	cagtgccttg	caccagcaga	cggtggaagtc	1950

cctgcccac	ctgcaggagg	taggtctcca	cggcaacccc	atccgctgtg	2000
actgtgtcat	ccgctgggcc	aatgccacgg	gcacccgtgt	ccgcttcac	2050
gagccgcaat	ccaccctgtg	tgcggagcct	ccggacctcc	agcgccctcc	2100
ggtccgtgag	gtgcccttcc	gggagatgac	ggaccactgt	ttgcccctca	2150
tctccccacg	aagcttcccc	ccaagcctcc	aggtagccag	tggagagagc	2200
atggtgctgc	attgccgggc	actggccgaa	cccgaacccg	agatctactg	2250
ggtcactcca	gctgggcttc	gactgacacc	tgcccatgca	ggcaggaggt	2300
accgggtgta	ccccgagggg	accctggagc	tgcggagggg	gacagcagaa	2350
gaggcagggc	tatacacctg	tgtggcccag	aacctgggtg	gggctgacac	2400
taagacggtt	agtgtggttg	tgggccgtgc	tctcctccag	ccaggcaggg	2450
acgaaggaca	ggggctggag	ctccgggtgc	aggagaccca	cccctatcac	2500
atcctgctat	cttgggtcac	cccacccaac	acagtgtcca	ccaacctcac	2550
ctggtccagt	gcctcctccc	tccggggcca	ggggggccaca	gctctggccc	2600
gcctgcctcg	gggaacccac	agctacaaca	ttacccgcct	ccttcaggcc	2650
acggagtact	gggcctgcct	gcaagtggcc	tttgctgatg	cccacacca	2700
gttggcttgt	gtatgggcca	ggaccaaaga	ggccacttct	tgccacagag	2750
ccttagggga	tcgctctggg	ctcattgcc	tcctggctct	cgctgtcctt	2800
ctcctggcag	ctgggctagc	ggcccacctt	ggcacaggcc	aaccagga	2850
gggtgtgggt	gggaggcggc	ctctccctcc	agcctgggct	ttctggggct	2900
ggagtgcccc	ttctgtccgg	gttgtgtctg	ctccctcgt	cctgcctgg	2950
aatccagga	ggaagctgcc	cagatcctca	gaaggggaga	cactgttgcc	3000
accattgtct	caaaattctt	gaagctcagc	ctgttctcag	cagtagagaa	3050
atcactagga	ctacttttta	ccaaaagaga	agcagtctgg	gccagatgcc	3100
ctgccaggaa	agggacatgg	accacgtgc	ttgaggctg	gcagctgggc	3150
caagacagat	ggggctttgt	ggccctgggg	gtgcttctgc	agccttgaaa	3200
aagttgcct	tacctctag	ggtcacctct	gctgccattc	tgaggaacat	3250

ctccaaggaa caggaggac tttggctaga gcctcctgcc tccccatctt 3300  
ctctctgccc agaggctcct gggcctggct tggctgtccc ctacctgtgt 3350  
ccccgggctg cacccttcc tcttctcttt ctctgtacag tctcagttgc 3400  
ttgctcttgt gcctcctggg caagggtga aggaggccac tccatctcac 3450  
ctcggggggc tgccctcaat gtgggagtga cccagccag atctgaagga 3500  
catttgggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550  
ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
aataaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly	1	5	10	15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro	20	25	30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

Asn Gln Leu Tyr	Arg Ile Ala Pro Arg	Ala Phe Ser Gly Leu Ser
155		160 165
Asn Leu Leu Arg	Leu His Leu Asn Ser	Asn Leu Leu Arg Ala Ile
170		175 180
Asp Ser Arg Trp	Phe Glu Met Leu Pro	Asn Leu Glu Ile Leu Met
185		190 195
Ile Gly Gly Asn	Lys Val Asp Ala Ile	Leu Asp Met Asn Phe Arg
200		205 210
Pro Leu Ala Asn	Leu Arg Ser Leu Val	Leu Ala Gly Met Asn Leu
215		220 225
Arg Glu Ile Ser	Asp Tyr Ala Leu Glu	Gly Leu Gln Ser Leu Glu
230		235 240
Ser Leu Ser Phe	Tyr Asp Asn Gln Leu	Ala Arg Val Pro Arg Arg
245		250 255
Ala Leu Glu Gln	Val Pro Gly Leu Lys	Phe Leu Asp Leu Asn Lys
260		265 270
Asn Pro Leu Gln	Arg Val Gly Pro Gly	Asp Phe Ala Asn Met Leu
275		280 285
His Leu Lys Glu	Leu Gly Leu Asn Asn	Met Glu Glu Leu Val Ser
290		295 300
Ile Asp Lys Phe	Ala Leu Val Asn Leu	Pro Glu Leu Thr Lys Leu
305		310 315
Asp Ile Thr Asn	Asn Pro Arg Leu Ser	Phe Ile His Pro Arg Ala
320		325 330
Phe His His Leu	Pro Gln Met Glu Thr	Leu Met Leu Asn Asn Asn
335		340 345
Ala Leu Ser Ala	Leu His Gln Gln Thr	Val Glu Ser Leu Pro Asn
350		355 360
Leu Gln Glu Val	Gly Leu His Gly Asn	Pro Ile Arg Cys Asp Cys
365		370 375
Val Ile Arg Trp	Ala Asn Ala Thr Gly	Thr Arg Val Arg Phe Ile
380		385 390
Glu Pro Gln Ser	Thr Leu Cys Ala Glu	Pro Pro Asp Leu Gln Arg
395		400 405
Leu Pro Val Arg	Glu Val Pro Phe Arg	Glu Met Thr Asp His Cys

	410		415		420
Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val					
	425		430		435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu					
	440		445		450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu					
	455		460		465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly					
	470		475		480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr					
	485		490		495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val					
	500		505		510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu					
	515		520		525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His					
	530		535		540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn					
	545		550		555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr					
	560		565		570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr					
	575		580		585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala					
	590		595		600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr					
	605		610		615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly					
	620		625		630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly					
	635		640		645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly					
	650		655		660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser					
	665		670		675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                                 680                                685                                690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                                 695                                700                                705

Leu Pro Pro Leu Ser Gln Asn Ser  
                                 710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag gcgctgtttg agaaggtgaa gaagttccgg acccatgtgg 50

aggaggggga cattgtgtac cgcctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcctcctcat catctgctac accgtctact acgtgcacaa 150

catcaagttc	gacgtggact	gcaccgtgga	cattgagagc	ctgacgggct	200
accgcaccta	ccgctgtgcc	caccccttgg	ccacactctt	caagatcctg	250
gcgtccttct	acatcagcct	agtcattctt	tacggcctca	tctgcatgta	300
cacactgtgg	tggatgctac	ggcgtccct	caagaagtac	tcgtttgagt	350
cgatccgtga	ggagagcagc	tacagcgaca	tccccgacgt	caagaacgac	400
ttcgcttca	tgctgcacct	cattgaccaa	tacgaccgc	tctactcaa	450
gcgttctgcc	gtcttcctgt	cggaggtgag	tgagaacaag	ctgcggcagc	500
tgaacctcaa	caacgagtgg	acgctggaca	agctccggca	gcggctcacc	550
aagaacgcgc	aggacaagct	ggagctgcac	ctgttcattg	tcagtggcat	600
ccctgacact	gtgtttgacc	tggtggagct	ggaggtcctc	aagctggagc	650
tgatccccga	cgtgaccatc	ccgccagca	ttgccagct	cacgggcctc	700
aaggagctgt	ggctctacca	cacagcggcc	aagattgaag	cgctgcgct	750
ggccttcctg	cgcgagaacc	tgcgggcgct	gcacatcaag	ttcaccgaca	800
tcaaggagat	cccgtgtgg	atctatagcc	tgaagacact	ggaggagctg	850
cacctgacgg	gcaacctgag	cgcggagaa	aaccgctaca	tcgtcatcga	900
cgggctgcgg	gagctcaaac	gcctcaaggt	gctgcggctc	aagagcaacc	950
taagcaagct	gccacaggtg	gtcacagatg	tgggcgtgca	cctgcagaag	1000
ctgtccatca	acaatgaggg	caccaagctc	atcgctctca	acagcctcaa	1050
gaagatggcg	aacctgactg	agctggagct	gatccgctgc	gacctggagc	1100
gcatccccc	ctccatcttc	agctccaca	acctgcagga	gattgacctc	1150
aaggacaaca	acctcaagac	catcgaggag	atcatcagct	tccagcacct	1200
gcaccgcctc	acctgcctta	agctgtggta	caaccacatc	gcctacatcc	1250
ccatccagat	cggcaacctc	accaacctgg	agcgctctca	cctgaaccgc	1300
aacaagatcg	agaagatccc	caccagctc	ttctactgcc	gcaagctgcg	1350
ctacctggac	ctcagccaca	acaacctgac	cttcctccct	gccgacatcg	1400
gcctcctgca	gaacctccag	aacctagcca	tcacggccaa	ccggatcgag	1450



acgctccctc	cggagctctt	ccagtgccgg	aagctgcggg	cctgcacct	1500
gggcaacaac	gtgctgcagt	cactgccctc	cagggtgggc	gagctgacca	1550
acctgacgca	gatcgagctg	cggggcaacc	ggctggagtg	cctgcctgtg	1600
gagctgggcg	agtgccact	gctcaagcgc	agcggcttgg	tggaggagga	1650
ggacctgttc	aacacactgc	cacccgaggt	gaaggagcgg	ctgtggaggg	1700
ctgacaagga	gcaggcctga	gcgaggccgg	cccagcacag	caagcagcag	1750
gaccgctgcc	cagtcctcag	gcccggaggg	gcaggcctag	cttctccag	1800
aactcccgga	cagccaggac	agcctcgcgg	ctgggcagga	gcctggggcc	1850
gcttgtgagt	caggccagag	cgagaggaca	gtatctgtgg	ggctggcccc	1900
ttttctccct	ctgagactca	cgtccccag	ggcaagtgct	tgtggaggag	1950
agcaagtctc	aagagcgcag	tatttgata	atcagggctc	cctccctgga	2000
ggccagctct	gccccagggg	ctgagctgcc	accagaggtc	ctgggacctt	2050
cactttagtt	cttggtattt	atttttctcc	atctcccacc	tccttcaccc	2100
agataactta	tacattccca	agaaagtcca	gccagatgg	aagggtgttca	2150
gggaaagggtg	ggctgccttt	tccccttgct	cttattttagc	gatgccgccg	2200
ggcatttaac	accacactgg	acttcagcag	agtgggtccg	ggcgaaccag	2250
ccatgggacg	gtcaccagc	agtgcggggc	tgggctctgc	ggtgcgggtcc	2300
acgggagagc	aggcctccag	ctggaaaggc	caggcctgga	gcttgccctc	2350
tcagtttttg	tggcagtttt	agttttttgt	tttttttttt	tttaatcaaa	2400
aaacaatttt	ttttaaaaaa	aagctttgaa	aatggatggg	ttgggtatta	2450
aaaagaaaaa	aaaaacttaa	aaaaaaaaag	acactaacgg	ccagtgagtt	2500
ggagtctcag	ggcaggggtg	cagtttcctt	tgagcaaagc	agccagacgt	2550
tgaactgtgt	ttcctttccc	tgggcgcagg	gtgcaggggtg	tcttcaggat	2600
ctgggtgtgac	cttggtccag	gagttctatt	tgttcctggg	gagggaggtt	2650
tttttgtttg	ttttttgggt	ttttttgggt	tcttgttttc	tttctcctcc	2700
atgtgtcttg	gcaggcactc	atttctgtgg	ctgtcggcca	gagggaatgt	2750
tctggagctg	ccaaggaggg	aggagactcg	ggttggctaa	tccccgatg	2800

aacggtgctc cattcgcacc tccccctcctc gtgcctgccc tgcctctcca 2850  
 cgcacagtgt taaggagcca agaggagcca cttegcccag actttgtttc 2900  
 cccacctcct gcggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950  
 cttccatcag cctgtcgcc acctggctct tcatgaagag cagacactta 3000  
 gaggctggtc gggaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050  
 ccaagccggt tcccgctcct ggcgcctgga gtgcacacag cccagtcggc 3100  
 acctggtggc tggaagccaa cctgctttag atcactcggg tccccacctt 3150  
 agaaggggtc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tcttaatgat tatgtccatc cgtctgtccg tccatttgtg 3250  
 ttttctgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccggt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400

a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10				15	
Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
			20						25				30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
			35						40				45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
			50						55				60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
			65						70				75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
			80						85				90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys

	95	100	105
Asn Asp Phe Ala	Phe Met Leu His Leu	Ile Asp Gln Tyr Asp	Pro
	110	115	120
Leu Tyr Ser Lys	Arg Phe Ala Val Phe	Leu Ser Glu Val Ser	Glu
	125	130	135
Asn Lys Leu Arg	Gln Leu Asn Leu Asn	Asn Glu Trp Thr Leu	Asp
	140	145	150
Lys Leu Arg Gln	Arg Leu Thr Lys Asn	Ala Gln Asp Lys Leu	Glu
	155	160	165
Leu His Leu Phe	Met Leu Ser Gly Ile	Pro Asp Thr Val Phe	Asp
	170	175	180
Leu Val Glu Leu	Glu Val Leu Lys Leu	Glu Leu Ile Pro Asp	Val
	185	190	195
Thr Ile Pro Pro	Ser Ile Ala Gln Leu	Thr Gly Leu Lys Glu	Leu
	200	205	210
Trp Leu Tyr His	Thr Ala Ala Lys Ile	Glu Ala Pro Ala Leu	Ala
	215	220	225
Phe Leu Arg Glu	Asn Leu Arg Ala Leu	His Ile Lys Phe Thr	Asp
	230	235	240
Ile Lys Glu Ile	Pro Leu Trp Ile Tyr	Ser Leu Lys Thr Leu	Glu
	245	250	255
Glu Leu His Leu	Thr Gly Asn Leu Ser	Ala Glu Asn Asn Arg	Tyr
	260	265	270
Ile Val Ile Asp	Gly Leu Arg Glu Leu	Lys Arg Leu Lys Val	Leu
	275	280	285
Arg Leu Lys Ser	Asn Leu Ser Lys Leu	Pro Gln Val Val Thr	Asp
	290	295	300
Val Gly Val His	Leu Gln Lys Leu Ser	Ile Asn Asn Glu Gly	Thr
	305	310	315
Lys Leu Ile Val	Leu Asn Ser Leu Lys	Lys Met Ala Asn Leu	Thr
	320	325	330
Glu Leu Glu Leu	Ile Arg Cys Asp Leu	Glu Arg Ile Pro His	Ser
	335	340	345
Ile Phe Ser Leu	His Asn Leu Gln Glu	Ile Asp Leu Lys Asp	Asn
	350	355	360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

caacaatgag ggcaccaagc 20

&lt;210&gt; 252

&lt;211&gt; 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50  
 gcgctctccc gtcccgcggt gggtgctgct gctgccgctg ctgctggggc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctgggtcatgt 250  
 ggcttcaggg cgggccaggc gggtctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtaggg actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatgggtggt 450  
 tcagacatga tgggtctcct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550  
 cagctggcat tggcttagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650  
 tgattcgggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800  
agaaatgatac attgaacaga acacagatgg ggtgaacttc tataacatct 850  
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
agatgcctta agccagctca tgaatggccc catcagaaaag aagctcaaaa 1000  
ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050  
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150  
tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200  
gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250  
taaattctttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300  
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450  
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550  
ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600  
taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10				15	

Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20						25				30	

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35						40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	80	85	90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	95	100	105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	110	115	120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	125	130	135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	140	145	150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	170	175	180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	200	205	210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	215	220	225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	230	235	240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly			

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

```

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50
tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250
ctcacggcgg cgactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```



cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450  
 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500  
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
 tacatcaaag aggatgaggc actgccatct cccacacccc tccaggaagt 600  
 tcaggctgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650  
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700  
 caaggcggga aggatgcctg cttcggtgac tcagggtggac ccttggcctg 750  
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800  
 gctgtgggtc gccaatcgg ccggtgtct acaccaatat cagccaccac 850  
 tttgagtgga tccagaagct gatggcccag agtggcatgt ccagccaga 900  
 cccctcctgg ccaactactct ttttccctct tctctgggct ctcccactcc 950  
 tggggccggt ctgagcctac ctgagcccat gcagcctggg gccactgcc 1000  
 agtcaggccc tggttctctt ctgtcttgtt tggttaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1				5					10					15

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
				20					25				30	

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
				35					40				45	

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
				50					55				60	

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
				65					70				75	

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
				80					85				90	

Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	95	100	105
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	110	115	120
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro	125	130	135
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr	140	145	150
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe	155	160	165
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	170	175	180
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln	185	190	195
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys	200	205	210
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	215	220	225
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	230	235	240
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	245	250	255
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	260	265	270
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	275	280	285
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	290	295	300
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val		305	310	

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

cccacgcgtc cgcgacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg	ctctttgccc	tcctcctctc	tggcaaatgc	agttacagcc	100
cggagcccga	ccagcggagg	acgctgcccc	caggctgggt	gtccctgggc	150
cgtgcggaac	ctgaggaaga	gctgagttct	acctttgccc	tgagacagca	200
gaatgtggaa	agactctcgg	agctgggtgca	ggctgtgtcg	gatcccagct	250
ctcctcaata	cggaaaatac	ctgaccctag	agaatgtggc	tgatctgggtg	300
aggccatccc	cactgaccct	ccacacgggtg	caaaaatggc	tcttgggcagc	350
cggagcccag	aagtgccatt	ctgtgatcac	acaggacttt	ctgacttgct	400
ggctgagcat	ccgacaagca	gagctgctgc	tccctggggc	tgagtttcat	450
cactatgtgg	gaggacctac	ggaaacccat	gttgtaaggt	ccccacatcc	500
ctaccagctt	ccacaggcct	tggcccccca	tgtggacttt	gtgggggggac	550
tgcaccgttt	tcccccaaca	tcctccctga	ggcaacgtcc	tgagccgcag	600
gtgacagggg	ctgtaggcct	gcatctgggg	gtaaccccct	ctgtgatccg	650
taagcgatac	aacttgacct	cacaagacgt	gggctctggc	accagcaata	700
acagccaagc	ctgtgcccag	ttcctggagc	agtatttcca	tgactcagac	750
ctggctcagt	tcctgcgcct	cttcgggtggc	aactttgcac	atcaggcatc	800
agtagcccg	gtggttgga	aacagggccg	gggcccgggc	gggattgagg	850
ccagtctaga	tgtgcagtac	ctgatgagtg	ctggtgccaa	catctccacc	900
tgggtctaca	gtagccctgg	ccggcatgag	ggacaggagc	ccttcctgca	950
gtggctcatg	ctgctcagta	atgagtcagc	cctgccacat	gtgcatactg	1000
tgagctatgg	agatgatgag	gactccctca	gcagcgcta	catccagcgg	1050
gtcaacactg	agctcatgaa	ggctgccgct	cgggggtctca	ccctgctctt	1100
cgctcaggt	gacagtgggg	ccgggtgttg	gtctgtctct	ggaagacacc	1150
agttccgccc	taccttcct	gcctccagcc	cctatgtcac	cacagtggga	1200
ggcacatcct	tccaggaacc	tttcctcatc	acaaatgaaa	ttgttgacta	1250
tatcagtggt	ggtggcttca	gcaatgtgtt	cccacggcct	tcataccagg	1300
aggaagctgt	aacgaagttc	ctgagctcta	gccccacct	gccaccatcc	1350
agttacttca	atgccagtgg	ccgtgcctac	ccagatgtgg	ctgcactttc	1400

tgatggctac tgggtggtca gcaacagagt gccattcca tgggtgtccg 1450  
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg cggccccct cttggctttc tcaacccaag 1550  
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600  
 atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggt 1650  
 cctggctggg atcctgtaac aggctgggga acaccaactt cccagctttg 1700  
 ctgaagactc tactcaacct ctgaccttt cctatcagga gagatggctt 1750  
 gtccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgga 1800  
 agccctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aacctgaaa tgcgtgagc ttgacttgac tcccaacct accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca tttttgaaat gcctctccct ccgcatctca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccaa ttcactgcaa ggagacctct actgtcaccg 2100  
 tttactcttt cctacctga catccagaaa caatggctc cagtgcatac 2150  
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttcctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300  
 tgtagatfff tgctcttctc agtttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaag taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1					5				10				15	

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

	20		25		30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	290	295	300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	305	310	315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	320	325	330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	335	340	345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

```
<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien
```

```
<400> 260
gccgcgcgct ctctcccggc gccacacact gtctgagcgg cgcagcgagc 50
cgcgggcccg gcgggctgct cggcgcgga cagtgtcgg catggcaggg 100
attccagggc tcctcttctt tctcttctt ctgctctgtg ctgttgggca 150
agtgagccct tacagtggcc cctggaaacc cacttggcct gcataccgcc 200
tcctgtgctg cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac ccagtggtca 300
taagggaact ccactgcca cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcctc 400
tacatctca gcagtagtgg agatggggcc caacaccgag actcaggggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actaccttt ctcaacatca 550
gtgaagtatt ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcttaaagc ccaagtttaa agatgggtggt 700
cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctctgtctaa 900
gcagctgcca gggggcagaa ttcaattctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctgggggt 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaaatta 1100
```

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gattttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200  
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggctctca tgttcttatt ttaggagagg 1300  
 ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactggttt gtgtatcata tcatatatca 1450  
 ttttaagcagt ttgaaggcat acttttgcag agaaataaaa aaaataactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1				5				10					15	

Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
			20					25					30	

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
			35					40					45	

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
			50					55					60	

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
			65					70					75	

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
			80					85					90	

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
			95					100					105	

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
			110					115					120	



Ser Gly Lys Ser	Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile	Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val	Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His	Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val	Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe	Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro	Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val	Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys	Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly	Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn	Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu	Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly	Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg	Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn	Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp	Cys Arg Glu Gly	380		

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
 ccatgggtgggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct cctgctgct gctggcgteg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca cactgcgca ggttctctgc tcaccagccg 300  
 ctgggtgatc actgctgcc actgtttcaa ggacaacctg aacaaaccat 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
 cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgt 500  
 ccatacagtt ctgagagcgg gtctgccca tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac cactgctgg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc ccaccctca gaccctgcag aagctgaagg 650  
 ttctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccatcactga ggacatgtg tgtgccggt acttgagggg 750  
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggtgt 850  
 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgctgg cgcgtcagg 950  
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000  
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100  
 aataggctca tctaccteta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc cgcggcccccac gaattccggc 1250  
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
 ataggtattt gtaaccctgc ccacatatct tattttattcc tccaatttca 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly Ser Ile Gln Asp Gly Val Pro Leu	Pro His Pro Gln Thr Leu
185	190 195
Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His	
200	205 210
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met	
215	220 225
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly	
230	235 240
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu	
245	250 255
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn	
260	265 270
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val	
275	280 285
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly	
290	295 300
Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala	
305	310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gtgc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 266

agctctagac caatgccagc ttcc 24

<210> 267

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 267

gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 268

ggggaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggctc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgatt gctggttagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gtcataca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctggcg actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100



[illegible]

ttctgaatgg gataccactc aaaggggtgaa gaggtcagct gtcctcctgt 1450  
 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500  
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650  
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
 tgccacaca gcatgtgcgc tctccctgag tgctgtgta gctggggatg 1750  
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtggggg aggcaggac gagggaagga aagtaactcc tgactctcca 1850  
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Pro	Leu	Leu
1				5					10				15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr
				20					25				30
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg
				35					40				45
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp
				50					55				60
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys
				65					70				75
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu
				80					85				90
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu
				95					100				105
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr
				110					115				120
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp
				125					130				135

Lys Thr Glu Arg	Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu	140	145	150
Gln Gly Val Glu	Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr	155	160	165
Glu Pro Pro Gly	Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly	170	175	180
Thr Pro Cys Ser	Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser	185	190	195
Leu Cys Glu Pro	Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro	200	205	210
Tyr Leu Val Thr	Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser	215	220	225
Asp Ser Arg Lys	Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile	230	235	240
Pro Ala Phe Leu	Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys	245	250	255
Ala Leu Pro Ala	Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr	260	265	270
Lys Asp Pro Pro	Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr	275	280	285
Thr Glu Val Pro	Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu	290	295	300
Asp Glu Glu Pro	Val Thr Phe Pro Lys Ser Thr His Val Pro Ile	305	310	315
Pro Lys Ser Ala	Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser	320	325	330
Arg Ser Pro Glu	Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly	335	340	345
Ala Arg Glu Leu	Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu	350	355	360
Ala Glu Leu Pro	Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro	365	370	375
Ala Gln Asp Lys	Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr	380	385	390
Gly His Thr Ser	Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser	395	400	405

```

<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 286
tcctgcagtt tcctgatgc 19

<210> 287
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 287
ctcatattgc acaccagtaa ttcg 24

<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 288
atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien

<400> 289
gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

```

tcatttctcca	agtttatgggtg	gacgtacttctc	tgttgtttctc	cctctgcttg	100
cttttttcaca	ttagcagacc	ggacttaagt	cacaacagat	tatctttcat	150
caaggcaagt	tccatgagcc	accttcaaag	ccttcgagaa	gtgaaactga	200
acaacaatga	attggagacc	attccaaatc	tgggaccagt	ctcggcaa	250
attacacttc	tctccttggc	tggaaacagg	attgttgaaa	tactccctga	300
acatctgaaa	gagtttcagt	cccttgaaac	tttggaacctt	agcagcaaca	350
atatttcaga	gctccaaact	gcatttccag	ccctacagct	caaatatctg	400
tatctcaaca	gcaaccgagt	cacatcaatg	gaacctgggt	attttgacaa	450
tttggccaac	acactccttg	tgttaaagct	gaacaggaac	cgaatctcag	500
ctatcccacc	caagatgttt	aaactgcccc	aactgcaaca	tctcgaattg	550
aaccgaaaca	agattaaaaa	tgtagatgga	ctgacattcc	aaggccttgg	600
tgctctgaag	tctctgaaaa	tgcaaagaaa	tggagtaacg	aaacttatgg	650
atggagcttt	ttggggggctg	agcaacatgg	aaattttgca	gctggaccat	700
aacaacctaa	cagagattac	caaaggctgg	ctttacggct	tgctgatgct	750
gcaggaactt	catctcagcc	aaaatgccat	caacaggatc	agccctgatg	800
cctgggagtt	ctgccagaag	ctcagtgagc	tggacctaac	tttcaatcac	850
ttatcaaggt	tagatgattc	aagcttcctt	ggcctaagct	tactaaatac	900
actgcacatt	gggaacaaca	gagtcagcta	cattgctgat	tgtgccttcc	950
ggggggctttc	cagtttaaag	actttggatc	tgaagaacaa	tgaaatttcc	1000
tggactattg	aagacatgaa	tgggtgctttc	tctgggcttg	acaaactgag	1050
gcgactgata	ctccaaggaa	atcggatccg	ttctattact	aaaaaagcct	1100
tcactggttt	ggatgcattg	gagcatctag	acctgagtga	caacgcaatc	1150
atgtctttac	aaggcaatgc	attttcacaa	atgaagaaac	tgcaacaatt	1200
gcattttaat	acatcaagcc	ttttgtgcga	ttgccagcta	aaatggctcc	1250
cacagtgggt	ggcggaaaaac	aactttcaga	gctttgtaaa	tgccagttgt	1300
gcccatacctc	agctgctaaa	aggaagaagc	atttttgctg	ttagcccaga	1350

tggctttgtg	tgtgatgatt	ttcccaaacc	ccagatcacg	gttcagccag	1400
aaacacagtc	ggcaataaaa	ggttccaatt	tgagtttcat	ctgctcagct	1450
gccagcagca	gtgattcccc	aatgactttt	gcttggaaaa	aagacaatga	1500
actactgcat	gatgctgaaa	tggaaaatta	tgcacacctc	cgggcccaag	1550
gtggcgaggt	gatggagtat	accaccatcc	ttcggctgcg	cgaggtggaa	1600
tttgccagtg	aggggaaata	tcagtgtgtc	atctccaatc	actttggttc	1650
atcctactct	gtcaaagcca	agcttacagt	aaatatgctt	ccctcattca	1700
ccaagacccc	catggatctc	accatccgag	ctggggccat	ggcacgcttg	1750
gagtgtgctg	ctgtggggca	cccagcccc	cagatagcct	ggcagaagga	1800
tgggggcaca	gacttcccag	ctgcacggga	gagacgcatg	catgtgatgc	1850
ccgaggatga	cgtgttcttt	atcgtggatg	tgaagataga	ggacattggg	1900
gtatacagct	gcacagctca	gaacagtgca	ggaagtattt	cagcaaatgc	1950
aactctgact	gtcctagaaa	caccatcatt	tttgcgcca	ctgttggaac	2000
gaactgtaac	caagggagaa	acagccgtcc	tacagtgcat	tgctggagga	2050
agccctcccc	ctaaactgaa	ctggaccaa	gatgatagcc	cattggtggt	2100
aaccgagagg	cacttttttg	cagcaggcaa	tcagcttctg	attattgtgg	2150
actcagatgt	cagtgatgct	gggaaataca	catgtgagat	gtctaacacc	2200
cttggcactg	agagaggaaa	cgtgcgcctc	agtgtgatcc	ccactccaac	2250
ctgcgactcc	cctcagatga	cagccccatc	gttagacgat	gacggatggg	2300
ccactgtggg	tgtcgtgatc	atagccgtgg	tttgctgtgt	ggtgggcacg	2350
tcactcgtgt	gggtggtcat	catataccac	acaaggcgga	ggaatgaaga	2400
ttgcagcatt	accaacacag	atgagaccaa	cttgccagca	gatattccta	2450
gttatttgtc	atctcagggg	acgttagctg	acaggcagga	tgggtacgtg	2500
tcttcagaaa	gtggaagcca	ccaccagttt	gtcacatctt	caggtgctgg	2550
atttttctta	ccacaacatg	acagtagtgg	gacctgccat	attgacaata	2600
gcagtgaagc	tgatgtggaa	gctgccacag	atctgttcct	ttgtccgttt	2650
ttgggatcca	caggccctat	gtattttgaag	ggaaatgtgt	atggctcaga	2700

tccttttgaa acatatcata caggttgcag tcctgaccca agaacagttt 2750  
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctaccca 2800  
 tgtttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850  
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900  
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950  
 agtgcaaadc cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000  
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag ctttttattt gaaagctcat 3100  
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaatc acatttgtac ctttaaacag acttttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250  
 tgagacccaaa ggaaaagctt aacatactac ctcaagttaa cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaacta 3450  
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500  
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600  
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650  
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25				30	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			



290					295					300				
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile
				305					310					315
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg
				320					325					330
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala
				335					340					345
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn
				350					355					360
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys
				365					370					375
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys
				380					385					390
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln
				395					400					405
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly
				410					415					420
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp
				425					430					435
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala
				440					445					450
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser
				455					460					465
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu
				470					475					480
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln
				485					490					495
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu
				500					505					510
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn
				515					520					525
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn
				530					535					540
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg
				545					550					555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560	565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575	580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590	595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605	610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620	625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665	670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740	745		750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

Tyr Val Ser Ser	Glu Ser Gly Ser	His His Gln Phe Val Thr Ser
815		820 825
Ser Gly Ala Gly	Phe Phe Leu Pro Gln	His Asp Ser Ser Gly Thr
830		835 840
Cys His Ile Asp	Asn Ser Ser Glu Ala	Asp Val Glu Ala Ala Thr
845		850 855
Asp Leu Phe Leu	Cys Pro Phe Leu Gly	Ser Thr Gly Pro Met Tyr
860		865 870
Leu Lys Gly Asn	Val Tyr Gly Ser Asp	Pro Phe Glu Thr Tyr His
875		880 885
Thr Gly Cys Ser	Pro Asp Pro Arg Thr	Val Leu Met Asp His Tyr
890		895 900
Glu Pro Ser Tyr	Ile Lys Lys Lys Glu	Cys Tyr Pro Cys Ser His
905		910 915
Pro Ser Glu Glu	Ser Cys Glu Arg Ser	Phe Ser Asn Ile Ser Trp
920		925 930
Pro Ser His Val	Arg Lys Leu Leu Asn	Thr Ser Tyr Ser His Asn
935		940 945
Glu Gly Pro Gly	Met Lys Asn Leu Cys	Leu Asn Lys Ser Ser Leu
950		955 960
Asp Phe Ser Ala	Asn Pro Glu Pro Ala	Ser Val Ala Ser Ser Asn
965		970 975
Ser Phe Met Gly	Thr Phe Gly Lys Ala	Leu Arg Arg Pro His Leu
980		985 990
Asp Ala Tyr Ser	Ser Phe Gly Gln Pro	Ser Asp Cys Gln Pro Arg
995		1000 1005
Ala Phe Tyr Leu	Lys Ala His Ser Ser	Pro Asp Leu Asp Ser Gly
1010		1015 1020
Ser Glu Glu Asp	Gly Lys Glu Arg Thr	Asp Phe Gln Glu Glu Asn
1025		1030 1035
His Ile Cys Thr	Phe Lys Gln Thr Leu	Glu Asn Tyr Arg Thr Pro
1040		1045 1050
Asn Phe Gln Ser	Tyr Asp Leu Asp Thr	
1055		

&lt;210&gt; 291

&lt;211&gt; 2906

<213> Homo Sapien

gggggagagga	attgaccatg	taaaaggaga	cttttttttt	tgggtggtggt	50	
ggctgttg	ggg	tgccttgcaa	aaatgaagga	tgcaggacgc	agctttctcc	100
tggaaccgaa	cgcaatggat	aaactgattg	tgcaagagag	aaggaagaac	150	
gaagcttttt	cttgtgagcc	ctggatctta	acacaaatgt	gtatatgtgc	200	
acacagggag	cattcaagaa	tgaataaac	cagagttaga	cccgcggggg	250	
ttggtgtgtt	ctgacataaa	taaataatct	taaagcagct	gttcccctcc	300	
ccacccccaa	aaaaaaggat	gattggaaat	gaagaaccga	ggattcacia	350	
agaaaaaagt	atgttcattt	ttctctataa	aggagaaagt	gagccaagga	400	
gatattttttg	gaatgaaaag	tttggggctt	ttttagtaaa	gtaaagaact	450	
ggtgtggtgg	tgttttctt	tctttttgaa	tttcccacia	gaggagagga	500	
aattaataat	acatctgcaa	agaaatttca	gagaagaaaa	gttgaccgcg	550	
gcagattgag	gcattgattg	ggggagagaa	accagcagag	cacagttgga	600	
tttgtgccta	tgttgactaa	aattgacgga	taattgcagt	tggatttttc	650	
ttcatcaacc	tcottttttt	taaattttta	ttccttttgg	tatcaagatc	700	
atgcgttttc	tcttgttctt	aaccacctgg	atttccatct	ggatgttgct	750	
gtgatcagtc	tgaataacaa	ctgtttgaat	tccagaagga	ccaacaccag	800	
ataaattatg	aatgttgaac	aagatgacct	tacatccaca	gcagataatg	850	
ataggtccta	ggtttaacag	ggccctattt	gacccctgc	ttgtggtgct	900	
gctggctctt	caacttcttg	tgggtggtgg	tctggtgcgg	gctcagacct	950	
gcccttctgt	gtgctcctgc	agcaaccagt	tcagcaaggt	gatttgtgtt	1000	
cggaaaaaac	tgcgtgaggt	tccggatggc	atctccacca	acacacggct	1050	
gctgaacctc	catgagaacc	aatccagat	catcaaagtg	aacagcttca	1100	
agcacttgag	gcacttgga	atcctacagt	tgagtaggaa	ccatatcaga	1150	
accattgaaa	ttggggcttt	caatggtctg	gcgaacctca	acactctgga	1200	
actctttgac	aatcgtctta	ctaccatccc	gaatggagct	tttgtatact	1250	

tgtctaaact	gaaggagctc	tggttgcgaa	acaaccccat	tgaaagcatc	1300
ccttcttatg	cttttaacag	aattccttct	ttgcgccgac	tagacttagg	1350
ggaattgaaa	agactttcat	acatctcaga	aggtgccttt	gaaggtctgt	1400
ccaacttgag	gtatttgaac	cttgccatgt	gcaaccttcg	ggaaatccct	1450
aacctcacac	cgctcataaa	actagatgag	ctggatcttt	ctgggaatca	1500
tttatctgcc	atcaggcctg	gctctttcca	gggtttgatg	caccttcaaa	1550
aactgtggat	gatacagtcc	cagattcaag	tgattgaacg	gaatgccttt	1600
gacaaccttc	agtcactagt	ggagatcaac	ctggcacaca	ataatctaac	1650
attactgcct	catgacctct	tcactccctt	gcatcatcta	gagcggatac	1700
atttacatca	caacccttgg	aactgtaact	gtgacatact	gtggctcagc	1750
tggtggtata	aagacatggc	cccctcgaac	acagcttggt	gtgcccgggtg	1800
taacactcct	cccaatctaa	aggggaggtg	cattggagag	ctcgaccaga	1850
attacttcac	atgctatgct	ccggtgattg	tggagcccc	tgcagacctc	1900
aatgtcactg	aaggcatggc	agctgagctg	aaatgtcggg	cctccacatc	1950
cctgacatct	gtatcttggg	ttactccaaa	tggaacagtc	atgacacatg	2000
gggcgtacaa	agtgcggata	gctgtgctca	gtgatggtac	gttaaatttc	2050
acaaatgtaa	ctgtgcaaga	tacaggcatg	tacacatgta	tggtgagtaa	2100
ttccgttggg	aatactactg	cttcagccac	cctgaatggt	actgcagcaa	2150
ccactactcc	tttctcttac	ttttcaaccg	tcacagtaga	gactatggaa	2200
ccgtctcagg	atgaggcacg	gaccacagat	aacaatgtgg	gtcccactcc	2250
agtggtcgac	tgggagacca	ccaatgtgac	cacctctctc	acaccacaga	2300
gcacaaggtc	gacagagaaa	accttcacca	tcccagtgac	tgatataaac	2350
agtgggatcc	caggaattga	tgaggtcatg	aagactacca	aaatcatcat	2400
tgggtgtttt	gtggccatca	cactcatggc	tgcagtgatg	ctgggtcattt	2450
tctacaagat	gaggaagcag	caccatcggc	aaaaccatca	cgcccccaaca	2500
aggactgttg	aaattattaa	tgtggatgat	gagattacgg	gagacacacc	2550

catggaaagc cacctgccc tgcctgctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcattgaa ccgttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750  
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1				5					10					15
Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
			20						25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
			35						40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
			50						55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
			65						70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
			80						85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
			95						100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
			110						115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
			125						130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
			140						145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

	155		160		165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp	410		415		420

Thr Gly Met Tyr	Thr Cys Met Val	Ser Asn Ser Val Gly Asn Thr	425	430	435
Thr Ala Ser Ala	Thr Leu Asn Val	Thr Ala Ala Thr Thr Thr Pro	440	445	450
Phe Ser Tyr Phe	Ser Thr Val Thr Val	Glu Thr Met Glu Pro Ser	455	460	465
Gln Asp Glu Ala	Arg Thr Thr Asp Asn	Asn Val Gly Pro Thr Pro	470	475	480
Val Val Asp Trp	Glu Thr Thr Asn Val	Thr Thr Ser Leu Thr Pro	485	490	495
Gln Ser Thr Arg	Ser Thr Glu Lys Thr	Phe Thr Ile Pro Val Thr	500	505	510
Asp Ile Asn Ser	Gly Ile Pro Gly Ile	Asp Glu Val Met Lys Thr	515	520	525
Thr Lys Ile Ile	Ile Gly Cys Phe Val	Ala Ile Thr Leu Met Ala	530	535	540
Ala Val Met Leu	Val Ile Phe Tyr Lys	Met Arg Lys Gln His His	545	550	555
Arg Gln Asn His	His Ala Pro Thr Arg	Thr Val Glu Ile Ile Asn	560	565	570
Val Asp Asp Glu	Ile Thr Gly Asp Thr	Pro Met Glu Ser His Leu	575	580	585
Pro Met Pro Ala	Ile Glu His Glu His	Leu Asn His Tyr Asn Ser	590	595	600
Tyr Lys Ser Pro	Phe Asn His Thr Thr	Thr Val Asn Thr Ile Asn	605	610	615
Ser Ile His Ser	Ser Val His Glu Pro	Leu Leu Ile Arg Met Asn	620	625	630
Ser Lys Asp Asn	Val Gln Glu Thr Gln	Ile	635	640	

&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

agccgacgct gctcaagctg caactctgtt gcagttggca gttcttttcg 50



gtttccctcc	tgctgttttg	gggcatgaaa	gggcttcgcc	gccgggagta	100
aaagaaggaa	ttgaccgggc	agcgcgaggg	aggagcgcgc	acgcgaccgc	150
gagggcgggc	gtgcaccctc	ggctggaagt	ttgtgccggg	ccccgagcgc	200
gcgccggctg	ggagcttcgg	gtagagacct	aggccgctgg	accgcgatga	250
gcgcgccgag	cctccgtgcg	cgccgcgcgg	ggttggggct	gctgctgtgc	300
gcggtgctgg	ggcgcgctgg	ccggtccgac	agcggcggtc	gcggggaact	350
cgggcagccc	tctggggtag	ccgccgagcg	cccatgcccc	actacctgcc	400
gctgcctcgg	ggacctgctg	gactgcagtc	gtaagcggct	agcgcgtctt	450
cccagaccac	tcccgtcctg	ggtcgctcgg	ctggacttaa	gtcacaacag	500
attatctttc	atcaaggcaa	gttccatgag	ccaccttcaa	agccttcgag	550
aagtgaact	gaacaacaat	gaattggaga	ccattccaaa	tctgggacca	600
gtctcggcaa	atattacact	tctctccttg	gctggaaaca	ggattgttga	650
aatactccct	gaacatctga	aagagtttca	gtcccttgaa	actttggacc	700
ttagcagcaa	caatatttca	gagctccaaa	ctgcatttcc	agccctacag	750
ctcaaatatc	tgtatctcaa	cagcaaccga	gtcacatcaa	tggaacctgg	800
gtattttgac	aatttgcca	acacactcct	tgtgttaaag	ctgaacagga	850
accgaatctc	agctatccca	ccaagatgt	ttaaactgcc	ccaactgcaa	900
catctcgaat	tgaaccgaaa	caagattaaa	aatgtagatg	gactgacatt	950
ccaaggcctt	ggtgctctga	agtctctgaa	aatgcaaaga	aatggagtaa	1000
cgaacttat	ggatggagct	ttttgggggc	tgagcaacat	ggaaattttg	1050
cagctggacc	ataacaacct	aacagagatt	accaaaggct	ggctttacgg	1100
cttgcctgat	ctgcaggaac	ttcatctcag	ccaaaatgcc	atcaacagga	1150
tcagccctga	tgcttgggag	ttctgccaga	agctcagtga	gctggacctt	1200
actttcaatc	acttatcaag	gtagatgat	tcaagcttcc	ttggcctaag	1250
cttactaaat	acactgcaca	ttgggaacaa	cagagtcagc	tacattgctg	1300
attgtgcctt	ccgggggctt	tccagtttaa	agactttgga	tctgaagaac	1350

aatgaaattt	cctggactat	tgaagacatg	aatggtgctt	tctctgggct	1400
tgacaaactg	aggcgactga	tactccaagg	aaatcggatc	cgttctatta	1450
ctaaaaaagc	cttcactgg	ttggatgcat	tggagcatct	agacctgagt	1500
gacaacgcaa	tcatgtcttt	acaaggcaat	gcattttcac	aaatgaagaa	1550
actgcaacaa	ttgcatttaa	atacatcaag	ccttttgtgc	gattgccagc	1600
taaaatggct	cccacagtgg	gtggcggaaa	acaactttca	gagctttgta	1650
aatgccagtt	gtgcccaccc	tcagctgcta	aaaggaagaa	gcatttttgc	1700
tgttagccca	gatggctttg	tgtgtgatga	ttttcccaa	cccagatca	1750
cggttcagcc	agaaacacag	tcggcaataa	aaggttccaa	tttgagtttc	1800
atctgctcag	ctgccagcag	cagtgattcc	ccaatgactt	ttgcttggaa	1850
aaaagacaat	gaactactgc	atgatgctga	aatggaaaat	tatgcacacc	1900
tccgggcccc	aggtggcgag	gtgatggagt	ataccaccat	ccttcggctg	1950
cgcgaggtgg	aatttgccag	tgaggggaaa	tatcagtgtg	tcatctcaa	2000
tcactttggt	tcatectact	ctgtcaaagc	caagcttaca	gtaaatatgc	2050
ttccctcatt	caccaagacc	cccattggatc	tcaccatccg	agctggggcc	2100
atggcacgct	tggagtgtgc	tgctgtgggg	caccagccc	cccagatagc	2150
ctggcagaag	gatgggggca	cagacttccc	agctgcacgg	gagagacgca	2200
tgcatgtgat	gcccgaggat	gacgtgttct	ttatcgtgga	tgtgaagata	2250
gaggacattg	gggtatacag	ctgcacagct	cagaacagtg	caggaagtat	2300
ttcagcaa	at	ctgtcctaga	aacaccatca	tttttgcggc	2350
cactgttgga	ccgaactgta	accaagggag	aaacagccgt	cctacagtgc	2400
attgctggag	gaagccctcc	ccctaaactg	aactggacca	aagatgatag	2450
cccattggtg	gtaaccgaga	ggcacttttt	tgcagcaggc	aatcagcttc	2500
tgattattgt	ggactcagat	gtcagtgatg	ctgggaaata	cacatgtgag	2550
atgtctaaca	cccttggcac	tgagagagga	aacgtgcgcc	tcagtgtgat	2600
ccccactcca	acctgcgact	cccctcagat	gacagcccca	tcgttagacg	2650
atgacggatg	ggccactgtg	ggtgtcgtga	tcatagccgt	ggtttgcgtg	2700

gtgggtgggca	cgtcactcgt	gtgggtggtc	atcatataacc	acacaaggcg	2750
gaggaatgaa	gattgcagca	ttaccaacac	agatgagacc	aacttgccag	2800
cagatattcc	tagttatttg	tcatctcagg	gaacgttagc	tgacaggcag	2850
gatgggtacg	tgtcttcaga	aagtggaagc	caccaccagt	ttgtcacatc	2900
ttcaggtgct	ggatttttct	taccacaaca	tgacagtagt	gggacctgcc	2950
atattgacaa	tagcagtga	gctgatgtgg	aagctgccac	agatctgttc	3000
ctttgtccgt	ttttgggatc	cacaggccct	atgtatttga	agggaaatgt	3050
gtatggctca	gacctttttg	aaacatatca	tacaggttgc	agtcctgacc	3100
caagaacagt	tttaatggac	cactatgagc	ccagttacat	aaagaaaaag	3150
gagtgctacc	catgtttctca	tccttcagaa	gaatcctgcg	aacggagcct	3200
cagtaatata	tcgtggcctt	cacatgtgag	gaagctactt	aacactagtt	3250
actctcacia	tgaaggacct	ggaatgaaaa	atctgtgtct	aaacaagtcc	3300
tcttttagatt	ttagtgcaaa	tccagagcca	gcgtcggttg	cctcgagtaa	3350
ttctttcatg	ggtacctttg	gaaaagctct	caggagacct	cacctagatg	3400
cctattcaag	ctttggacag	ccatcagatt	gtcagccaag	agccttttat	3450
ttgaaagctc	attcttcccc	agacttggac	tctgggtcag	aggaagatgg	3500
gaaagaaagg	acagattttc	aggaagaaaa	tcacatttgt	acctttaaac	3550
agactttaga	aaactacagg	actccaaatt	ttcagtctta	tgacttggac	3600
acatagactg	aatgagacca	aaggaaaagc	ttaacatact	acctcaagtg	3650
aactttttatt	taaaagagag	agaatcttat	gtttttttaa	tgagattatg	3700
aatttttaaaa	ggataaaaaat	gctttattta	tacagatgaa	ccaaaattac	3750
aaaaagttat	gaaaattttt	atactgggaa	tgatgctcat	ataagaatac	3800
cttttttaaac	tatttttttaa	ctttgtttta	tgcaaaaaag	tatcttacgt	3850
aaattaatga	tataaatcat	gattattttta	tgtattttta	taatgccaga	3900
tttctttttta	tggaaaatga	gttactaaag	catttttaaat	aatacctgcc	3950
ttgtaccatt	ttttaaatag	aagttacttc	attatatattt	gcacattata	4000

tttaataaaaa tgtgtcaatt tgaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4050

aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met	Ser	Ala	Pro	Ser	Leu	Arg	Ala	Arg	Ala	Ala	Gly	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly	20	25	30	
Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg	35	40	45	
Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys	50	55	60	
Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp	65	70	75	
Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys	80	85	90	
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	95	100	105	
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	110	115	120	
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	125	130	135	
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	140	145	150	
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	155	160	165	
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	170	175	180	
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	185	190	195	
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	200	205	210	
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn				

	215		220		225
Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala					
	230		235		240
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met					
	245		250		255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu					
	260		265		270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly					
	275		280		285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn					
	290		295		300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu					
	305		310		315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser					
	320		325		330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn					
	335		340		345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser					
	350		355		360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile					
	365		370		375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg					
	380		385		390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala					
	395		400		405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn					
	410		415		420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys					
	425		430		435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys					
	440		445		450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln					
	455		460		465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly					
	470		475		480

Arg	Ser	Ile	Phe	Ala 485	Val	Ser	Pro	Asp	Gly 490	Phe	Val	Cys	Asp	Asp 495
Phe	Pro	Lys	Pro	Gln 500	Ile	Thr	Val	Gln	Pro 505	Glu	Thr	Gln	Ser	Ala 510
Ile	Lys	Gly	Ser	Asn 515	Leu	Ser	Phe	Ile	Cys 520	Ser	Ala	Ala	Ser	Ser 525
Ser	Asp	Ser	Pro	Met 530	Thr	Phe	Ala	Trp	Lys 535	Lys	Asp	Asn	Glu	Leu 540
Leu	His	Asp	Ala	Glu 545	Met	Glu	Asn	Tyr	Ala 550	His	Leu	Arg	Ala	Gln 555
Gly	Gly	Glu	Val	Met 560	Glu	Tyr	Thr	Thr	Ile 565	Leu	Arg	Leu	Arg	Glu 570
Val	Glu	Phe	Ala	Ser 575	Glu	Gly	Lys	Tyr	Gln 580	Cys	Val	Ile	Ser	Asn 585
His	Phe	Gly	Ser	Ser 590	Tyr	Ser	Val	Lys	Ala 595	Lys	Leu	Thr	Val	Asn 600
Met	Leu	Pro	Ser	Phe 605	Thr	Lys	Thr	Pro	Met 610	Asp	Leu	Thr	Ile	Arg 615
Ala	Gly	Ala	Met	Ala 620	Arg	Leu	Glu	Cys	Ala 625	Ala	Val	Gly	His	Pro 630
Ala	Pro	Gln	Ile	Ala 635	Trp	Gln	Lys	Asp	Gly 640	Gly	Thr	Asp	Phe	Pro 645
Ala	Ala	Arg	Glu	Arg 650	Arg	Met	His	Val	Met 655	Pro	Glu	Asp	Asp	Val 660
Phe	Phe	Ile	Val	Asp 665	Val	Lys	Ile	Glu	Asp 670	Ile	Gly	Val	Tyr	Ser 675
Cys	Thr	Ala	Gln	Asn 680	Ser	Ala	Gly	Ser	Ile 685	Ser	Ala	Asn	Ala	Thr 690
Leu	Thr	Val	Leu	Glu 695	Thr	Pro	Ser	Phe	Leu 700	Arg	Pro	Leu	Leu	Asp 705
Arg	Thr	Val	Thr	Lys 710	Gly	Glu	Thr	Ala	Val 715	Leu	Gln	Cys	Ile	Ala 720
Gly	Gly	Ser	Pro	Pro 725	Pro	Lys	Leu	Asn	Trp 730	Thr	Lys	Asp	Asp	Ser 735
Pro	Leu	Val	Val	Thr 740	Glu	Arg	His	Phe	Phe 745	Ala	Ala	Gly	Asn	Gln 750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr
				755					760					765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val
				770					775					780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met
				785					790					795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val
				800					805					810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val
				815					820					825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys
				830					835					840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				845					850					855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly
				860					865					870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser
				875					880					885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr
				890					895					900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr
				905					910					915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr
				920					925					930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His
				935					940					945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr
				950					955					960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His
				965					970					975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp
				980					985					990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn
				995					1000					1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

<210> 295  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 295  
 ggaaccgaat ctcagcta 18

<210> 296  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 296  
 cctaaactga actggacca 19

<210> 297  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe



<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 300  
gggtcttggt gaatgagg 18

<210> 301  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

cccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 306

actccaagga aatcggatcc gtcc 24

<210> 307

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 308

actccaagga aatcggatcc gttc 24

<210> 309

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 309

gccttcactg gtttggatgc attggagcat ctagacctga gtagacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

caaaacttgc gtcgcggaga gcgcccagct tgacttgaat ggaaggagcc 50  
cgagcccgcg gagcgcagct gagactgggg gagcgcgttc ggctgtggg 100  
gcgcccgtcg gcgcccgggg gcagcaggga aggggaagct gtggtctgcc 150  
ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200  
ccgtccccta tccctccttt atatagaaac cttccacact ggaaggcag 250  
cggcgaggca ggagggtca tggtagcaa ggaggccggc tgatctgcag 300  
gcgcacagca ttccgagttt acagattttt acagatacca aatggaaggc 350  
gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcg 400

atctgactcg	gcacccccctg	caggcaccat	ggcccagagc	cgggtgctgc	450
tgctcctgct	gctgctgccg	ccacagctgc	acctgggacc	tgtgcttgcc	500
gtgagggccc	caggatttgg	ccgaagtggc	ggccacagcc	tgagccccga	550
agagaacgaa	tttgcgagg	aggagccggt	gctggtactg	agccctgagg	600
agcccggggc	tggcccagcc	gcggtcagct	gccccgaga	ctgtgcctgt	650
tcccaggagg	gcgtcgtgga	ctgtggcggt	attgacctgc	gtgagttccc	700
gggggacctg	cctgagcaca	ccaaccacct	atctctgcag	aacaaccagc	750
tggaaaagat	ctaccctgag	gagctctccc	ggctgcaccg	gctggagaca	800
ctgaacctgc	aaaacaaccg	cctgacttcc	cgagggctcc	cagagaaggc	850
gtttgagcat	ctgaccaacc	tcaattacct	gtacttggcc	aataacaagc	900
tgaccttggc	accccgcttc	ctgccaaacg	ccctgatcag	tgtggacttt	950
gctgccaact	atctcaccaa	gatctatggg	ctcacctttg	gccagaagcc	1000
aaacttgagg	tctgtgtacc	tgcacaacaa	caagctggca	gacgccgggc	1050
tgccggacaa	catgttcaac	ggctccagca	acgtcgaggt	cctcatcctg	1100
tccagcaact	tcctgcgcca	cgtgcccag	cacctgccgc	ctgccctgta	1150
caagctgcac	ctcaagaaca	acaagctgga	gaagatcccc	ccgggggcct	1200
tcagcgagct	gagcagcctg	cgcgagctat	acctgcagaa	caactacctg	1250
actgacgagg	gcctggacaa	cgagaccttc	tggaagctct	ccagcctgga	1300
gtacctggat	ctgtccagca	acaacctgtc	tcggggtcca	gctgggctgc	1350
cgcgcagcct	ggtgctgctg	cacttgagga	agaacgccat	ccggagcgtg	1400
gacgcgaatg	tgctgacccc	catccgcagc	ctggagtacc	tgctgctgca	1450
cagcaaccag	ctgcgggagc	agggcatcca	cccactggcc	ttccaggggc	1500
tcaagcggtt	gcacacggtg	cacctgtaca	acaacgcgct	ggagcgcgtg	1550
cccagtggcc	tgctcgcgcg	cgtgcgccac	ctcatgatcc	tgcacaacca	1600
gatcacaggc	attggccgcg	aagactttgc	caccacctac	ttcctggagg	1650
agctcaacct	cagctacaac	cgcataccca	gcccacaggt	gcaccgcgac	1700

gccttcgcga	agctgcgcct	gctgcgctcg	ctggacctgt	cgggcaaccg	1750
gctgcacacg	ctgccacctg	ggctgcctcg	aaatgtccat	gtgctgaagg	1800
tcaagcgcaa	tgagctggct	gccttggcac	gaggggcgct	ggcgggcatg	1850
gctcagctgc	gtgagctgta	cctcaccagc	aaccgactgc	gcagccgagc	1900
cctggggccc	cgtgcctggg	tggacctcgc	ccatctgcag	ctgctggaca	1950
tcgccgggaa	tcagctcaca	gagatccccg	aggggctccc	cgagtcactt	2000
gagtacctgt	acctgcagaa	caacaagatt	agtgcggtgc	ccgccaatgc	2050
cttcgactcc	acgcccaccc	tcaaggggat	ctttctcagg	tttaacaagc	2100
tggctgtggg	ctccgtggtg	gacagtgcct	tccggaggct	gaagcacctg	2150
caggtcttgg	acattgaagg	caacttagag	tttggtgaca	tttccaagga	2200
ccgtggccgc	ttggggaagg	aaaaggagga	ggaggaagag	gaggaggagg	2250
aggaagagga	aacaagatag	tgacaaggtg	atgcagatgt	gacctaggat	2300
gatggaccgc	cggactcttt	tctgcagcac	acgcctgtgt	gctgtgagcc	2350
ccccactctg	ccgtgctcac	acagacacac	ccagctgcac	acatgaggca	2400
tcccacatga	cacgggctga	cacagtctca	tatccccacc	ccttcccacg	2450
gcgtgtccca	cggccagaca	catgcacaca	catcacacc	tcaaacaccc	2500
agctcagcca	cacacaacta	ccctccaaac	caccacagtc	tctgtcacac	2550
ccccactacc	gctgccacgc	cctctgaatc	atgcagggaa	gggtctgccc	2600
ctgccctggc	acacacaggc	accattcccc	tccccctgct	gacatgtgta	2650
tgcgatatga	tacacaccac	acacacacac	atgcacaagt	catgtgcgaa	2700
cagccctcca	aagcctatgc	cacagacagc	tcttgcccca	gccagaatca	2750
gccatagcag	ctcgccgtct	gcctgttcca	tctgtccgtc	cgttccctgg	2800
agaagacaca	agggtatcca	tgctctgtgg	ccaggtgcct	gccaccctct	2850
ggaactcaca	aaagctggct	tttattcctt	tcccatccta	tggggacagg	2900
agccttcagg	actgctggcc	tggcctggcc	caccctgctc	ctccaggtgc	2950
tgggcagtca	ctctgctaag	agtccctccc	tgccacgccc	tggcaggaca	3000
caggcacttt	tccaatgggc	aagcccagtg	gaggcaggat	gggagagccc	3050

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100  
 ctgggctgag ccagggagga aggaccagc tgcacctagg agacaccttt 3150  
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200  
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250  
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 311  
 gcattggccg cgagactttg cc 22

<210> 312  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 312  
 gcggccacgg tccttggaat tg 22

<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 313  
 tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314  
 <211> 3003  
 <212> DNA  
 <213> Homo Sapien

<400> 314  
 gggagggggc tccggggcgc gcgcagcaga cctgctccgg ccgcgcgcct 50  
 cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggtctg 100

gggttcctcg	agactctcag	agggggcgct	cccatcggcg	cccaccacc	150
caacctgttc	ctcgcgcgcc	actgcgctgc	gccccaggac	ccgctgcccc	200
acatggattt	tctcctggcg	ctggtgctgg	tatcctcgct	ctacctgcag	250
gcggccgcgc	agttcgacgg	gaggtggccc	aggcaaatag	tgtcatcgat	300
tggcctatgt	cgttatggtg	ggaggattga	ctgctgctgg	ggctgggctc	350
gccagtcttg	gggacagtgt	cagcctgtgt	gccaaccacg	atgcaaacat	400
ggtgaatgta	tcggggccaaa	caagtgcaag	tgtcatcctg	gttatgctgg	450
aaaaacctgt	aatcaagatc	taaatgagtg	tggcctgaag	ccccggccct	500
gtaagcacag	gtgcatgaac	acttacggca	gctacaagtg	ctactgtctc	550
aacggatata	tgctcatgcc	ggatggttcc	tgctcaagtg	ccctgacctg	600
ctccatggca	aactgtcagt	atggctgtga	tgttgttaaa	ggacaaatac	650
ggtgccagtg	cccatcccct	ggcctgcacc	tggctcctga	tgggaggacc	700
tgtgtagatg	ttgatgaatg	tgctacagga	agagcctcct	gccctagatt	750
taggcaatgt	gtcaacactt	ttgggagcta	catctgcaag	tgtcataaag	800
gcttcgatct	catgtatatt	ggaggcaaat	atcaatgtca	tgacatagac	850
gaatgctcac	ttggtcagta	tcagtgcagc	agctttgctc	gatgttataa	900
cgtacgtggg	tcctacaagt	gcaaattgtaa	agaaggatac	cagggtgatg	950
gactgacttg	tgtgtatatc	ccaaaagtta	tgattgaacc	ttcaggtcca	1000
attcatgtac	caaagggaaa	tggtaccatt	ttaaagggtg	acacaggaaa	1050
taataattgg	attcctgatg	ttggaagtac	ttggtggcct	ccgaagacac	1100
catatatctc	tcctatcatt	accaacaggc	ctacttctaa	gccaacaaca	1150
agacctacac	caaagccaac	accaattcct	actccaccac	caccaccacc	1200
cctgccaaca	gagctcagaa	cacctctacc	acctacaacc	ccagaaaggc	1250
caaccaccgg	actgacaact	atagcaccag	ctgccagtac	acctccagga	1300
gggattacag	ttgacaacag	ggtacagaca	gaccctcaga	aaccagagg	1350
agatgtgttc	agtgttctgg	tacacagttg	taattttgac	catggacttt	1400

gtggatggat	cagggagaaa	gacaatgact	tgactggga	accaatcagg	1450
gaccagcag	gtggacaata	tctgacagt	tcggcagcca	aagccccagg	1500
gggaaaagct	gcacgcttg	tgctacctct	cggccgcctc	atgcattcag	1550
gggacctgtg	cctgtcattc	aggcacaagg	tgacggggct	gcactctggc	1600
acactccagg	tgtttgtgag	aaaacacggt	gcccacggag	cagccctgtg	1650
gggaagaaat	ggtggccatg	gctggaggca	aacacagatc	accttgcgag	1700
gggctgacat	caagagcgaa	tcacaaagat	gattaaaggg	ttggaaaaaa	1750
agatctatga	tggaaaatta	aaggaactgg	gattattgag	cctggagaag	1800
agaagactga	ggggcaaacc	attgatgggt	ttcaagtata	tgaagggttg	1850
gcacagagag	ggtggcgacc	agctgttctc	catatgcact	aagaatagaa	1900
caagaggaaa	ctggcttaga	ctagagtata	agggagcatt	tcttggcagg	1950
ggccattggt	agaatacttc	ataaaaaaag	aagtgtgaaa	atctcagtat	2000
ctctctctct	ttctaaaaaa	ttagataaaa	atttgtctat	ttaagatggg	2050
taaagatggt	cttaccceaag	gaaaagtaac	aaattataga	atttcccaaa	2100
agatgttttg	atcctactag	tagtatgcag	tgaaaatctt	tagaactaaa	2150
taatttgga	aaggcttaat	ttaggcattt	ccctcttgac	ctcctaattg	2200
agagggattg	aaaggggaag	agcccaccaa	atgctgagct	cactgaaata	2250
tctctccctt	atggcaatcc	tagcagtatt	aaagaaaaaa	ggaaactatt	2300
tattccaaat	gagagtatga	tggacagata	ttttagtatc	tcagtaatgt	2350
cctagtgtgg	cgggtggtttt	caatgtttct	tcatggtaaa	ggtataagcc	2400
tttcatttgt	tcaatggatg	atgtttcaga	tttttttttt	tttaagagat	2450
ccttcaagga	acacagttca	gagagatttt	catcgggtgc	attctctctg	2500
cttcgtgtgt	gacaagttat	cttggctgct	gagaaagagt	gccctgcccc	2550
acaccggcag	acctttcctt	cacctcatca	gtatgattca	gtttctctta	2600
tcaattggac	tctcccaggt	tccacagaac	agtaatattt	tttgaacaat	2650
aggtacaata	gaaggctctc	tgtcatttaa	cctggtaaag	gcagggctgg	2700
agggggaaaa	taaatcatta	agcctttqag	taacggcaga	atatatggct	2750



gtagatccat ttttaatggt tcatttcctt tatgggcata taactgcaca 2800  
gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgcaa 2850  
tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
catcttggtt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000  
aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu	1	5	10	15
Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val	20	25	30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

Thr	Cys	Val	Asp	Val 170	Asp	Glu	Cys	Ala	Thr 175	Gly	Arg	Ala	Ser	Cys 180
Pro	Arg	Phe	Arg	Gln 185	Cys	Val	Asn	Thr	Phe 190	Gly	Ser	Tyr	Ile	Cys 195
Lys	Cys	His	Lys	Gly 200	Phe	Asp	Leu	Met	Tyr 205	Ile	Gly	Gly	Lys	Tyr 210
Gln	Cys	His	Asp	Ile 215	Asp	Glu	Cys	Ser	Leu 220	Gly	Gln	Tyr	Gln	Cys 225
Ser	Ser	Phe	Ala	Arg 230	Cys	Tyr	Asn	Val	Arg 235	Gly	Ser	Tyr	Lys	Cys 240
Lys	Cys	Lys	Glu	Gly 245	Tyr	Gln	Gly	Asp	Gly 250	Leu	Thr	Cys	Val	Tyr 255
Ile	Pro	Lys	Val	Met 260	Ile	Glu	Pro	Ser	Gly 265	Pro	Ile	His	Val	Pro 270
Lys	Gly	Asn	Gly	Thr 275	Ile	Leu	Lys	Gly	Asp 280	Thr	Gly	Asn	Asn	Asn 285
Trp	Ile	Pro	Asp	Val 290	Gly	Ser	Thr	Trp	Trp 295	Pro	Pro	Lys	Thr	Pro 300
Tyr	Ile	Pro	Pro	Ile 305	Ile	Thr	Asn	Arg	Pro 310	Thr	Ser	Lys	Pro	Thr 315
Thr	Arg	Pro	Thr	Pro 320	Lys	Pro	Thr	Pro	Ile 325	Pro	Thr	Pro	Pro	Pro 330
Pro	Pro	Pro	Leu	Pro 335	Thr	Glu	Leu	Arg	Thr 340	Pro	Leu	Pro	Pro	Thr 345
Thr	Pro	Glu	Arg	Pro 350	Thr	Thr	Gly	Leu	Thr 355	Thr	Ile	Ala	Pro	Ala 360
Ala	Ser	Thr	Pro	Pro 365	Gly	Gly	Ile	Thr	Val 370	Asp	Asn	Arg	Val	Gln 375
Thr	Asp	Pro	Gln	Lys 380	Pro	Arg	Gly	Asp	Val 385	Phe	Ser	Val	Leu	Val 390
His	Ser	Cys	Asn	Phe 395	Asp	His	Gly	Leu	Cys 400	Gly	Trp	Ile	Arg	Glu 405
Lys	Asp	Asn	Asp	Leu 410	His	Trp	Glu	Pro	Ile 415	Arg	Asp	Pro	Ala	Gly 420
Gly	Gln	Tyr	Leu	Thr	Val	Ser	Ala	Ala	Lys	Ala	Pro	Gly	Gly	Lys

	425		430		435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly					
	440		445		450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser					
	455		460		465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala					
	470		475		480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln					
	485		490		495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg					
	500		505		

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtgc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggaccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

<400> 319

cttcttttgaa	aaggattatc	acctgatcag	gttctctctg	catttgcccc	50
tttagattgt	gaaatgtggc	tcaaggctct	cacaactttc	ctttcctttg	100
caacaggtgc	ttgctcgggg	ctgaagggtg	cagtgccatc	acacactgtc	150
catggcgta	gaggtcaggc	cctctaccta	cccgtccact	atggcttcca	200
cactccagca	tcagacatcc	agatcatatg	gctatttgag	agaccccaca	250
caatgccc	atacttactg	ggctctgtga	ataagtctgt	ggttcctgac	300
ttggaatacc	aacacaagtt	caccatgatg	ccacccaatg	catctctgct	350
tatcaaccca	ctgcagttcc	ctgatgaagg	caattacatc	gtgaagggtc	400
acattcaggg	aaatggaact	ctatctgcc	gtcagaagat	acaagtcacg	450
gttgatgatc	ctgtcacaaa	gccagtgggtg	cagattcatc	ctccctctgg	500
ggctgtggag	tatgtgggga	acatgaccct	gacatgccat	gtggaagggg	550
gcactcggct	agcttaccaa	tggctaaaaa	atgggagacc	tgtccacacc	600
agctccacct	actccttttc	tccccaaaac	aatacccttc	atattgctcc	650
agtaaccaag	gaagacattg	ggaattacag	ctgcctgggtg	aggaaccctg	700
tcagtgaat	ggaaagtgat	atcattatgc	ccatcatata	ttatggacct	750
tatggacttc	aagtgaattc	tgataaaggg	ctaaaagtag	gggaagtgtt	800
tactgttgac	cttggaagg	ccatcctatt	tgattgttct	gctgattctc	850
atccccccaa	cacctactcc	tggattagga	ggactgacaa	tactacatat	900
atcattaagc	atgggcctcg	cttagaagtt	gcactctgaga	aagtagccca	950
gaagacaatg	gactatgtgt	gctgtgctta	caacaacata	accggcaggc	1000
aagatgaaac	tcatttcaca	gttatcatca	cttccgtagg	actggagaag	1050
cttgcacaga	aaggaaaatc	attgtcacct	ttagcaagta	taactggaat	1100
atcactat	ttgattatat	ccatgtgtct	tctcttccta	tggaaaaaat	1150
atcaacccta	caaagttata	aaacagaaac	tagaaggcag	gccagaaaca	1200
gaatacacga	aagctcaaac	atcttcaggc	catgaagatg	ctctggatga	1250

cttcggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300  
 ggattccaag caggtctggt ccagcctctg attgtgtatc ggggcaagat 1350  
 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400  
 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450  
 ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaactctgg 1500  
 aatcagtga gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
 tgcagaatag aggcatttat gcaaattgaa ctgcagggtt ttcagcatat 1600  
 acacaatgtc ttgtgcaaca gaaaaacatg ttgggggaaat attcctcagt 1650  
 ggagagtcgt tctcatgctg acggggagaa cgaaagtgc aggggtttcc 1700  
 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750  
 acactttcac tatcatcaac actgagacta tcctgtctca cctacaaatg 1800  
 tggaaacttt acattgttcg atttttcagc agactttggt ttattaaatt 1850  
 tttattagtg ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
 ttctatcttg ttatttgtac aacaaagtaa taaggatggg tgtcacaaaa 1950  
 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttataaa 2100  
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15
Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30
Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45
His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro 65	Lys	Tyr	Leu	Leu	Gly 70	Ser	Val	Asn	Lys	Ser 75
Val	Val	Pro	Asp	Leu 80	Glu	Tyr	Gln	His	Lys 85	Phe	Thr	Met	Met	Pro 90
Pro	Asn	Ala	Ser	Leu 95	Leu	Ile	Asn	Pro	Leu 100	Gln	Phe	Pro	Asp	Glu 105
Gly	Asn	Tyr	Ile	Val 110	Lys	Val	Asn	Ile	Gln 115	Gly	Asn	Gly	Thr	Leu 120
Ser	Ala	Ser	Gln	Lys 125	Ile	Gln	Val	Thr	Val 130	Asp	Asp	Pro	Val	Thr 135
Lys	Pro	Val	Val	Gln 140	Ile	His	Pro	Pro	Ser 145	Gly	Ala	Val	Glu	Tyr 150
Val	Gly	Asn	Met	Thr 155	Leu	Thr	Cys	His	Val 160	Glu	Gly	Gly	Thr	Arg 165
Leu	Ala	Tyr	Gln	Trp 170	Leu	Lys	Asn	Gly	Arg 175	Pro	Val	His	Thr	Ser 180
Ser	Thr	Tyr	Ser	Phe 185	Ser	Pro	Gln	Asn	Asn 190	Thr	Leu	His	Ile	Ala 195
Pro	Val	Thr	Lys	Glu 200	Asp	Ile	Gly	Asn	Tyr 205	Ser	Cys	Leu	Val	Arg 210
Asn	Pro	Val	Ser	Glu 215	Met	Glu	Ser	Asp	Ile 220	Ile	Met	Pro	Ile	Ile 225
Tyr	Tyr	Gly	Pro	Tyr 230	Gly	Leu	Gln	Val	Asn 235	Ser	Asp	Lys	Gly	Leu 240
Lys	Val	Gly	Glu	Val 245	Phe	Thr	Val	Asp	Leu 250	Gly	Glu	Ala	Ile	Leu 255
Phe	Asp	Cys	Ser	Ala 260	Asp	Ser	His	Pro	Pro 265	Asn	Thr	Tyr	Ser	Trp 270
Ile	Arg	Arg	Thr	Asp 275	Asn	Thr	Thr	Tyr	Ile 280	Ile	Lys	His	Gly	Pro 285
Arg	Leu	Glu	Val	Ala 290	Ser	Glu	Lys	Val	Ala 295	Gln	Lys	Thr	Met	Asp 300
Tyr	Val	Cys	Cys	Ala 305	Tyr	Asn	Asn	Ile	Thr 310	Gly	Arg	Gln	Asp	Glu 315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu

	320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly	335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp	350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly	365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His	380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe	395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro	410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr	425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu	440	445	450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatacctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50  
 cctgggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
 tggatgatag aattttatgc cccgtgggtgc cctgcttgtc aaaatcttca 200  
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
 ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300  
 ataactgctc ttcctactat ttatcattgt aaagatgggtg aatttaggcg 350  
 ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400  
 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
 gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
 gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
 ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650  
 accacagcca taccatacc cttcaaaaaa attattatca gaatctgcac 700  
 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750  
 tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
 gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
 cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900  
 aagattgac attttgtttg gtttgaagtg aactgtgact tttttgaata 950  
 ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000



acataaaaagc	actaggtata	caagtttgaa	atatgattta	agcacagtat	1050
gatgggttaa	atagttctct	aatttttgaa	aaatcgtgcc	aagcaataag	1100
atztatgtat	atttgtttaa	taataaccta	tttcaagtct	gagttttgaa	1150
aatttacatt	tcccaagtat	tgcattattg	aggtatttaa	gaagattatt	1200
ttagagaaaa	atatttctca	tttgatataa	tttttctctg	tttcaactgtg	1250
tgaaaaaaag	aagatatttc	ccataaatgg	gaagtttgcc	cattgtctca	1300
agaaatgtgt	atttcagtga	caatttcgtg	gtcttttttag	aggtatattc	1350
caaaatttcc	ttgtattttt	aggttatgca	actaataaaa	actaccttac	1400
attaattaat	tacagttttc	tacacatggg	aatacaggat	atgctactga	1450
tttaggaagt	ttttaagttc	atgggtattct	cttgattcca	acaaagtttg	1500
attttctctt	gtatttttct	tacttactat	gggttacatt	ttttattttt	1550
caaattggat	gataatttct	tggaaacatt	ttttatgttt	tagtaaacag	1600
tatttttttg	ttgtttcaaa	ctgaagttta	ctgagagatc	catcaaattg	1650
aacaatctgt	tgtaatttaa	aattttggcc	acttttttca	gattttacat	1700
cattcttgct	gaacttcaac	ttgaaattgt	tttttttttc	tttttggatg	1750
tgaaggtgaa	cattcctgat	ttttgtctga	tgtgaaaaag	ccttgggtatt	1800
ttacattttg	aaaattcaaa	gaagcttaat	ataaaagttt	gcattctact	1850
caggaaaaag	catcttcttg	tatatgtctt	aatgtatttt	ttgtcctcat	1900
atacagaaag	ttcttaattg	attttacagt	ctgtaatgct	tgatgtttta	1950
aaataataac	atttttatat	tttttaaaag	acaaacttca	tattatcctg	2000
tgttcttttc	tgactggtaa	tattgtgtgg	gatttccacag	gtaaaagtca	2050
gtaggatgga	acatttttagt	gtattttttac	tccttaaaga	gctagaatac	2100
atagttttca	ccttaaaaga	agggggaaaa	tcataaatac	aatgaatcaa	2150
ctgaccatta	cgtagtagac	aatttctgta	atgtccccct	ctttctaggc	2200
tctgttgctg	tgtgaatcca	ttagattttac	agtatcgtaa	tatacaagtt	2250
ttcttttaaag	ccctctcctt	tagaatttaa	aatattgtac	cattaaagag	2300
tttggatgtg	taacttggtga	tgccttagaa	aaatataccta	agcacaaaaat	2350

aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val  
1 5 10 15

Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn  
20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly  
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

	215		220		225									
Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu
				230					235					240
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu
				245					250					255
Gly	Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser
				260					265					270
Leu	Gly	Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser					
				275					280					

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcagggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctgggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgccatacaa ctggtgaagc ggctaaacac 450

agactggcct gcgctggagg accttgtcct gcaggactca gctgcaggtt 500

ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550

gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600

ggaccagggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggccgctc ggccatacat 700

gaaggggact attatcatac ggtgttgttg atggagcagg tgctaaagca 750

gcttgatgcc	ggggaggagg	ccaccacaa	caagtcacag	gtgctggact	800
acctcagcta	tgctgtcttc	cagttgggtg	atctgcaccg	tgccctggag	850
ctcaccgc	gctgtcttc	ccttgacca	agccacgaac	gagctggagg	900
gaatctgcgg	tactttgagc	agttattgga	ggaagagaga	gaaaaaacgt	950
taacaaatca	gacagaagct	gagctagcaa	ccccagaagg	catctatgag	1000
aggcctgtgg	actacctgcc	tgagagggat	gtttacgaga	gcctctgtcg	1050
tggggaggggt	gtcaaaactga	caccccgtag	acagaagagg	cttttctgta	1100
ggtaccacca	tggcaacagg	gccccacagc	tgctcattgc	cccttcaaa	1150
gaggaggacg	agtgggacag	ccgcacatc	gtcaggtact	acgatgtcat	1200
gtctgatgag	gaaatcgaga	ggatcaagga	gatcgcaaaa	cctaaacttg	1250
cacgagccac	cgttcgtgat	ccaagacag	gagtcctcac	tgtcgccagc	1300
taccgggttt	ccaaaagctc	ctggctagag	gaagatgatg	accctgttgt	1350
ggcccagta	aatcgtcgga	tgcagcatat	cacagggtta	acagtaaaga	1400
ctgcagaatt	gttacagggt	gcaaattatg	gagtgggagg	acagtatgaa	1450
ccgcacttcg	acttctctag	gcgacctttt	gacagcgggc	tcaaaacaga	1500
ggggaatagg	ttagcgacgt	ttcttaacta	catgagtgat	gtagaagctg	1550
gtggtgccac	cgtcttcct	gatctggggg	ctgcaatttg	gcctaagaag	1600
ggtacagctg	tgttctggta	caacctcttg	cggagcgggg	aagggtgacta	1650
ccgaacaaga	catgctgcct	gcctgtgct	tgtgggctgc	aagtgggtct	1700
ccaataagtg	gttccatgaa	cgaggacagg	agttcttgag	accttggtga	1750
tcaacagaag	ttgactgaca	tccttttctg	tccttccct	tcctggctct	1800
tcagcccatg	tcaacgtgac	agacaccttt	gtatgttct	ttgtatgttc	1850
ctatcaggct	gatttttggg	gaaatgaatg	tttgtctgga	gcagagggag	1900
accatactag	ggcgactcct	gtgtgactga	agtcccagcc	cttccattca	1950
gcctgtgcc	tccttgggc	caaggctagg	atcaaagtgg	ctgcagcaga	2000
gttagctgtc	tagcgctag	caaggctcct	ttgtacctca	ggtgttttag	2050
gtgtgagatg	tttcagtga	ccaaagtct	gataccttgt	ttacatgttt	2100

cctaccagaa aaaaaaaaaa 2168

<211> 533

<213> Homo Sapien

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val  
1 5 10 15

Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met  
20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys  
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile  
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu  
200 205 210

Asp Tyr Leu Ser	Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu	Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly	Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu	Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu	Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val	Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg	Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala	Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp	Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu	Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala	Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr	Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val	Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr	Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly	Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp	Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn	Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp	Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
 485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
 500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
 515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
 530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe



<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

<400> 338  
gcagtattga gttttacttc ctctctttt tagtggaaga cagaccataa 50  
tcccagtggt agtgaaattg attgtttcat ttattaccgt tttggctggg 100  
ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gacccaggt tctctggta aaactgaaag 250  
cctactactg gcctgggtgcc catcaatcca ttgatccttg aggctgtgcc 300  
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgcggccagc gttccctc atcttagggc tgtctctggg 400  
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
cccctactac agggacccca acaagcccta caagaagggt ctcaggactc 600  
ggtagatcca gacagagctg ggctcccggt agcgggttgc ggtggctgtc 650  
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
ggtggcccat cacttcctc ggttactcta cttcactggg cagcgggggg 750  
cccgggctcc agcagggatg caggtgggtg tcatgggga tgagcggccc 800

gcctgggtca	tgtcagagac	cctgcgccac	cttcacacac	actttggggc	850
cgactacgac	tgggttcttca	tcatgcagga	tgacacatat	gtgcaggccc	900
cccgctggc	agcccttgct	ggccacctca	gcatcaacca	agacctgtac	950
ttaggcggg	cagaggagtt	cattggcgca	ggcgagcagg	cccgtactg	1000
tcatgggggc	tttggctacc	tgttgtcacg	gagtctcctg	cttcgtctgc	1050
ggccacatct	ggatggctgc	cgaggagaca	ttctcagtgc	ccgtcctgac	1100
gagtggcttg	gacgctgcct	cattgactct	ctgggcgtcg	gctgtgtctc	1150
acagcaccag	gggcagcagt	atcgctcatt	tgaactggcc	aaaaataggg	1200
accctgagaa	ggaagggagc	tgggctttcc	tgagtgcctt	cgccgtgcac	1250
cctgtctccg	aaggtaccct	catgtaccgg	ctccacaaac	gcttcagcgc	1300
tctggagttg	gagcgggctt	acagtgaaat	agaacaactg	caggctcaga	1350
tccggaacct	gaccgtgctg	acccccgaag	gggaggcagg	gctgagctgg	1400
cccgttgggc	tccctgctcc	tttcacacca	cactctcgct	ttgaggtgct	1450
gggctgggac	tacttcacag	agcagcacac	cttctcctgt	gcagatgggg	1500
ctcccaagtg	cccactacag	ggggctagca	gggcggacgt	gggtgatgcg	1550
ttggagactg	ccctggagca	gctcaatcgg	cgctatcagc	cccgcctgcg	1600
cttcagaag	cagcgactgc	tcaacggcta	tggcgcttc	gaccagcac	1650
ggggcatgga	gtacaccctg	gacctgctgt	tggaatgtgt	gacacagcgt	1700
gggcaccggc	gggccctggc	tgcagggtc	agcctgctgc	ggccactgag	1750
ccgggtggaa	atcctaccta	tgccctatgt	cactgaggcc	acccgagtgc	1800
agctggtgct	gccactcctg	gtggctgaag	ctgctgcagc	ccgggctttc	1850
ctcgaggcgt	ttgcagccaa	tgtcctggag	ccacgagaac	atgcattgct	1900
caccctgttg	ctggctctacg	ggccacgaga	aggtggccgt	ggagctccag	1950
acccatttct	tgggggtgaag	gctgcagcag	cggagttaga	gcgacggtac	2000
cctgggacga	ggctggcctg	gctcgctgtg	cgagcagagg	ccccttccca	2050
ggtgcgactc	atggacgtgg	tctcgaagaa	gcaccctgtg	gacactctct	2100

tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150  
 tgtcgcatga atgccatctc tggctggcag gccttctttc cagtccattt 2200  
 ccaggagttc aatcctgccc tgtcaccaca gagatcaccc ccaggggccc 2250  
 cgggggctgg ccctgacccc cctcccccctc ctgggtgctga cccctcccgg 2300  
 ggggctccta taggggggag atttgaccgg caggcttctg cggagggctg 2350  
 cttctacaac gctgactacc tggcggcccg agcccggtg gcaggtgaac 2400  
 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450  
 gttttcctcc ggttctcagg gctccacctc tttcgggccg tagagccagg 2500  
 gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcaagtgaag 2550  
 aactctacca ccgctgccgc ctacagcaacc tggaggggct agggggccgt 2600  
 gccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650  
 gccgcctgg gggccctaac ctcatcactt ttcctttgtc tgcctcagcc 2700  
 ccaggaaggg caaggcaaga tgggtggacag atagagaatt gttgctgtat 2750  
 tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
1				5					10				15	
Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
				20					25				30	
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
				35					40				45	
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
				50					55				60	
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
				65					70				75	
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
				80					85				90	
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala

[illegible]

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

Ser	Pro	Gln	Arg	Ser	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Gly	Pro	Asp
				635					640					645
Pro	Pro	Ser	Pro	Pro	Gly	Ala	Asp	Pro	Ser	Arg	Gly	Ala	Pro	Ile
				650					655					660
Gly	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr
				665					670					675
Asn	Ala	Asp	Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu
				680					685					690
Ala	Gly	Gln	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met
				695					700					705
Asp	Val	Phe	Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val
				710					715					720
Glu	Pro	Gly	Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro
				725					730					735
Arg	Leu	Ser	Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu
				740					745					750
Glu	Gly	Leu	Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu
				755					760					765
Gln	Glu	Gln	Ala	Asn	Ser	Thr								
				770										

&lt;210&gt; 340

&lt;211&gt; 1572

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 340

```

cggagtggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50
tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100
ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

```

```
<210> 341
<211> 318
<212> PRT
<213> Homo Sapien
```

&lt;400&gt; 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
1				5					10					15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
				20					25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
				35					40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
				50					55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
				65					70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
				80					85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
				95					100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
				110					115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
				125					130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
				140					145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
				155					160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
				170					175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
				185					190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
				200					205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
				215					220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
				230					235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
				245					250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys



	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn Gly	Leu Thr Pro Asn Gln			
	275		280		285
Met His Val Met	Met Tyr Gly Val Tyr Arg	Leu Arg Ala Phe Gly			
	290		295		300
His Ile Phe Asn	Asp Ala Leu Val Phe	Leu Pro Pro Asn Gly	Ser		
	305		310		315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatt acgactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 350  
 ggattctaatacgcactcact atagggcggc gatgtccact ggggctac 48  
  
 <210> 351  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 351  
 ctatgaaatt aaccctcact aaaggacga ggaagatggg cggatggt 48  
  
 <210> 352  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 352  
 ggattctaatacgcactcact atagggcacc cacgcgtccg gctgctt 47  
  
 <210> 353  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 353  
 ctatgaaatt aaccctcact aaaggacgg gggacaccac ggaccaga 48  
  
 <210> 354  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 354  
 ggattctaatacgcactcact atagggcttg ctgcggtttt tgttcctg 48  
  
 <210> 355  
 <211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 355

ctatgaaatt aaccctcact aaagggagct gccgatccca ctggtatt 48

<210> 356

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 356

ggattctaatacgcactcactatagggcggaacctggccggcctctg 46

<210> 357

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 357

ctatgaaatt aaccctcact aaagggagcc cgggcacgtgt ctcagtta 48

<210> 358

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

ggattctaatacgcactcactatagggcggaagatggcgaaggaggag 47

<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 359

ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48

<210> 360  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 360  
ggattctaatac gactcact atagggtgt gctttcattc tgccagta 48

<210> 361  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 361  
ctatgaaatt aacctcact aaaggagg tacaattaag gggtagat 48

<210> 362  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 362  
ggattctaatac gactcact atagggccg cctcgctcct gctcctg 47

<210> 363  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaatt aacctcact aaaggagga ttgccgcac ctcacag 48

<210> 364  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 364

ggatttctaatacgaactcactatagggccccctctgccttcctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaattaacctcactaaagggagtgtggccgcgattatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggatttctaatacgaactcactatagggcgcgatggcagcgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaattaacctcactaaagggacagacggggcagagggagtg 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggatttctaatacgaactcactatagggccaggaggcgtgaggagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggatttctaatt acgactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggatttctaatt acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

ggattctaatacgactcactatagggccagctacccgcaggaggagg 47

<211> 48

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<211> 997

<213> Homo Sapien

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaaagag 50

agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100

aaaaaatgaa ttcattctaaa tcatctgaaa cacaatgcac agagagagga 150

tgcttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200

atttctcagt gcctgtttca tcaccagatg tgtttgtgaca tttcgcacatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagaq 300

ctctcctgct acaattatgg atcaggttca gtcaagaatt qttgtccatt 350

gaactgggaa tattttcaat ccaqctgcta cttcttttct actgacacca 400

tttctgggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450

gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccaggtt qtcgagggtc 550

agtggcaatg ggtggacggc acacctttga caaagtctct qagcttctcg 600

gatgtagggg agcccaacaa catagctacc ctggaggact qtqccaccat 650

gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700

tcaattattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750



```
<210> 377
<211> 219
<212> PRT
<213> Homo Sapien
```

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly
1				5					10					15
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro
				20					25					30
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35					40					45
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50					55					60
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
				65					70					75
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
				80					85					90
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
				95					100					105
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
				110					115					120
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
				125					130					135
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
				140					145					150
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
				155					160					165
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
				170					175					180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
                                   185                                  190                                  195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
                                   200                                  205                                  210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
                                   215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

<210> 382  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
ggccttgacg acaaccgt 18

<210> 383  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 384  
cagctgccct tccccaacca 20

<210> 385  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 385  
catcaagcgc ctctacca 18

<210> 386  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386

cacaaactcg aactgcttct g 21

<210> 387

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

gggccatcac agctccct 18

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gggatgtggt gaacacagaa ca 22

<210> 389

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 389

tgccagctgc atgctgccag tt 22

<210> 390

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcaggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggctttggta gt 22

<210> 398  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc cccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 400  
gcaaattcag ggctcactag aga 23

<210> 401  
<211> 29

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 401  
cacagagcat ttgtccatca gcagttcag 29

<210> 402  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 402  
ggcagagact tccagtcact ga 22

<210> 403  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 403  
gccaaaggtg gtgtagata gg 22

<210> 404  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
caggccccct tgatctgtac ccca 24

<210> 405  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 405  
gggacgtgct tctacaagaa cag 23

<210> 406  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
caggcttaca atgttatgat cagaca 26

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
tattcagagt tttccattgg cagtgccagt t 31

<210> 408  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
tctacatcag cctctctgcg c 21

<210> 409  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 409  
cgatcttctc caccaggag cgg 23

<210> 410  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 410



gccaggcctc acattcgt 18

<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

ctccctgaat ggcagcctga gca 23

<210> 412

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

aggtgtttat taaggccta cgct 24

<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cagagcagag ggtgccttg 19

<210> 414

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 414

tggcggagtc ccctcttggc t 21

<210> 415

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaaccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 420  
 tgtctgcctc agccccagga agg 23

<210> 421  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 421  
 tctgtccacc atcttgcctt g 21

<210> 422  
 <211> 3554  
 <212> DNA  
 <213> Homo Sapien

<400> 422  
 gggactacaa gccgcgccgc gctgccgctg gccctcagc aaccctcgac 50  
 atggcgctga ggccggccacc gcgactccgg ctctgcgctc ggctgcctga 100  
 cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
 tcaaatccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
 ctgtcttgca tcattacgga ttgcgagaca agtgacccca ggatcgagtg 250  
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
 ttcaggggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
 aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
 cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450  
 ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500  
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
 ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600  
 ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650  
 acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700  
 ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt	ctatgacctg	aacattggcg	gaattattgg	gggggttctg	800
gttgtccttg	ctgtactggc	cctgatcacg	ttgggcatct	gctgtgcata	850
cagacgtggc	tacttcatca	acaataaaca	ggatggagaa	agttacaaga	900
accaggggaa	accagatgga	gttaactaca	tccgcactga	cgaggagggc	950
gacttcagac	acaagtcatc	gtttgtgatc	tgagacccgc	ggtgtggctg	1000
agagcgcaca	gagcgcacgt	gcacatacct	ctgctagaaa	ctcctgtcaa	1050
ggcagcgaga	gctgatgcac	tccgacagag	ctagacactc	attcagaagc	1100
ttttcgtttt	ggccaaagtt	gaccactact	cttcttactc	taacaagcca	1150
catgaataga	agaatttttc	tcaagatgga	cccggtaa	ataaccacaa	1200
ggaagcgaaa	ctgggtgctg	tactgagtt	gggttcctaa	tctgtttctg	1250
gcctgattcc	cgcatgagta	ttaggggtgat	cttaaagagt	ttgctcacgt	1300
aaacgcccgt	gctgggccct	gtgaagccag	catgttcacc	actggtcggt	1350
cagcagccac	gacagcacca	tgtgagatgg	cgagggtggct	ggacagcacc	1400
agcagcgcac	cccggcggga	accagaaaa	ggcttcttac	acagcagcct	1450
tacttcatcg	gccacagac	accaccgcag	tttcttctta	aaggctctgc	1500
tgatcggtgt	tgcagtgtcc	attgtggaga	agctttttgg	atcagcattt	1550
tgtaaaaaca	accaaataca	ggaaggtaaa	ttggttgctg	gaagagggat	1600
cttgctgag	gaaccctgct	tgtccaacag	ggtgtcagga	tttaaggaaa	1650
accttcgtct	taggctaagt	ctgaaatggt	actgaaatat	gcttttctat	1700
gggtcttggt	tattttataa	aattttacat	ctaaattttt	gctaaggatg	1750
tattttgatt	attgaaaaga	aaatttctat	ttaaactgta	aatatatatt	1800
catacaatgt	taaataacct	atTTTTTTaa	aaaagttcaa	cttaaggtag	1850
aagttccaag	ctactagtgt	taaattggaa	aatatcaata	attaagagta	1900
ttttacccaa	ggaatcctct	catggaagtt	tactgtgatg	ttccttttct	1950
cacacaagtt	ttagcctttt	tcacaaggga	actcatactg	tctacacatc	2000
agaccatagt	tgcttaggaa	accttttaaaa	attccagtta	aqcaatqttq	2050

aaatcagttt	gcatctcttc	aaaagaaacc	tctcaggtta	gctttgaact	2100
gcctcttctc	gagatgacta	ggacagtctg	taccagagg	ccaccagaa	2150
gccctcagat	gtacatacac	agatgccagt	cagctcctgg	ggttgcgcca	2200
ggcgcccccg	ctctagctca	ctgttgccct	gctgtctgcc	aggaggccct	2250
gccatccttg	ggccctggca	gtggctgtgt	cccagtgagc	ttactcacg	2300
tggcccttgc	ttcatccagc	acagctctca	ggtgggcact	gcagggacac	2350
tgggtgtcttc	catgtagegt	cccagctttg	ggctcctgta	acagacctct	2400
ttttggttat	ggatggctca	caaaataggg	cccccaatgc	tatttttttt	2450
ttttaagttt	gtttaattat	ttgttaagat	tgtctaaggc	caaaggcaat	2500
tgcgaaatca	agtctgtcaa	gtacaataac	atttttaaaa	gaaaatggat	2550
cccactgttc	ctcttttgcca	cagagaaagc	accagacgc	cacaggctct	2600
gtcgcatttc	aaaacaaacc	atgatggagt	ggcggccagt	ccagcctttt	2650
aaagaacgtc	aggtggagca	gccaggtgaa	aggcctggcg	gggaggaaag	2700
tgaaacgcct	gaatcaaaag	cagttttcta	attttgactt	taaatttttc	2750
atccgcggga	gacactgctc	ccatttgctg	ggggacatta	gcaacatcac	2800
tcagaagcct	gtgttcttca	agagcaggtg	ttctcagcct	cacatgccct	2850
gccgtgctgg	actcaggact	gaagtgtgtg	aaagcaagga	gctgctgaga	2900
aggagcactc	cactgtgtgc	ctggagaatg	gctctcacta	ctcaccttgt	2950
ctttcagctt	ccagtgtctt	gggtttttta	tactttgaca	gctttttttt	3000
aattgcatac	atgagactgt	gttgactttt	tttagttatg	tgaaacactt	3050
tgccgcaggc	cgctggcag	aggcaggaaa	tgctccagca	gtggctcagt	3100
gtccctgggt	gtctgctgca	tggcatcctg	gatgcttagc	atgcaagttc	3150
cctccatcat	tgccaccttg	gtagagaggg	atggctcccc	accctcagcg	3200
ttggggattc	acgctccagc	ctccttcttg	gttgtcatag	tgatagggtta	3250
gccttattgc	cccctcttct	tataccctaa	aaccttctac	actagtgccca	3300
tgggaaccag	gtctgaaaaa	gtagagagaa	gtgaaagtag	agtctgggaa	3350
gtagctgcct	ataactgaga	ctagacggaa	aaggaataact	cgtgtatttt	3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450  
gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500  
caccgtaatt tggcatttgt ttaacctcat ttataaaaagc ttcaaaaaaa 3550  
ccca 3554

<210> 423

<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu	1	5	10	15
Pro	Asp	Phe	Phe	Leu	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly	20	25	30	
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	65	70	75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	80	85	90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val	95	100	105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val	125	130	135	
Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	140	145	150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	155	160	165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	170	175	180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	185	190	195	

His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
				200					205					210
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
				215					220					225
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
				230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
				245					250					255
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					